

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2003, 19:43:59 ; Search time 8.74286 Seconds
(without alignments)
2096.859 Million cell updates/sec

Title: US-09-497-967-6

Perfect score: 2342

Sequence: 1 MKYNILLIILISLFINELRA.....STTFKFLSISLLFISFYLL 442

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	213.5	9.1	713	1 TSA4_GIALA	P21849 giardia lam
2	202.5	8.6	3718	1 LMA5_MOUSE	Q61001 mus musculus
3	198	8.5	3084	1 LMA1_MOUSE	P19137 mus musculus
4	191	8.2	3110	1 LMA2_MOUSE	P24043 homo sapien
5	189	8.1	5376	1 ZAN_MOUSE	O88799 mus musculus
6	187	8.0	328	1 C170_GIALA	P15759 giardia lam
7	182	7.8	667	1 TS11_GIALA	Q03185 giardia lam
8	182	7.8	3695	1 LMA5_HUMAN	O15230 homo sapien
9	181.5	7.7	3075	1 LMA1_HUMAN	P25391 homo sapien
10	181	7.7	687	1 VS41_GIALA	P92127 giardia lam
11	178	7.6	3106	1 LMA2_MOUSE	Q60675 mus musculus
12	177.5	7.6	1607	1 LMGI_MOUSE	P02468 mus musculus
13	175	7.5	1587	1 LMGI_HUMAN	O9Y806 homo sapien
14	173	7.4	1790	1 LMGI_MOUSE	P11046 drosophila
15	172.5	7.4	1581	1 LMGI_MOUSE	Q9R086 mus musculus
16	172	7.3	913	1 PKK5_HUMAN	Q92824 homo sapien
17	171	7.3	1576	1 YK83_CAEEL	P41951 caenorhabdi
18	169.5	7.2	1169	1 YK82_YEAST	P36170 saccharomyc
19	169	7.2	1877	1 PKK5_MOUSE	Q04592 mus musculus
20	168.5	7.2	1696	1 PKK5_BRACL	O9N115 branchiostoc
21	166.5	7.1	1557	1 LML1_CAEEL	Q18823 caenorhabdi
22	165.5	7.1	1680	1 FUR2_DROME	P30432 drosophila
23	165.5	7.1	1700	1 BAR3_CHITE	Q03376 chironomus
24	165.5	7.1	3712	1 LMA_DROME	Q00174 drosophila
25	162.5	6.9	2704	1 G168_PARPR	P17053 paramesium
26	160	6.8	1609	1 LMGI_HUMAN	P11047 homo sapien
27	158.5	6.8	600	1 SP96_DICDI	P14328 dictyosteli
28	158	6.7	1246	1 YMV2_CAEEL	P34504 caenorhabdi
29	157	6.7	790	1 ANP_NOTCO	P24856 notothenia
30	156.5	6.7	2713	1 G156_PARPR	P13837 paramesium
31	156	6.7	1192	1 LMGI_MOUSE	Q61092 mus musculus
32	154.5	6.6	1786	1 LMB1_MOUSE	P02469 mus musculus
33	154.5	6.6	2556	1 NTC1_HUMAN	P46531 homo sapien

34	152.5	6.5	2471	1 NTC2_RAT	Q9QW30 rattus norv
35	151.5	6.5	3224	1 RBP2_HUMAN	P49792 homo sapien
36	150.5	6.4	1193	1 LMGI_MOUSE	Q13753 homo sapien
37	149	6.4	2437	1 NTC1_BRARE	P46530 brachydanio
38	147.5	6.3	2470	1 NTC2_MOUSE	O35516 mus musculus
39	146.5	6.3	1799	1 LMB2_MOUSE	Q61292 mus musculus
40	146	6.2	1797	1 VGLX_HSVB	P28968 equine herp
41	145.5	6.2	1786	1 LMB1_HUMAN	P07942 homo sapien
42	144.5	6.2	2531	1 NTC1_MOUSE	Q01705 mus musculus
43	143.5	6.1	2569	1 LMA3_MOUSE	Q61789 mus musculus
44	143	6.1	2524	1 NOTC_XENLA	P21783 xenopus lae
45	142.5	6.1	1877	1 PKK5_RAT	P41413 rattus norv

ALIGNMENTS

RESULT 1

TSA4_GIALA
ID TSA4_GIALA STANDARD; PRT; 713 AA.
AC P21849;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Major surface-labeled trophozoite antigen 417 precursor.
GN TSA 417.
OS Giardia lamblia (Giardia intestinalis).
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=5741;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 30957 / WB;
RX MEDLINE=90280395; PubMed=2352929;
RA Gillin F.D., Hagblom P., Harwood J., Alely S.B., Reiner D.S.,
RA McCaffery M., So M., Guiney D.G.;
RT "Isolation and expression of the gene for a major surface protein of
Giardia lamblia.";
RL Giardia lamblia.;
RL Proc. Natl. Acad. Sci. U.S.A. 87:4463-4467(1990).
RN [2]
RP SEQUENCE OF 480-620 FROM N.A.
RC STRAIN=AD-1;
RX MEDLINE=93314970; PubMed=8325510;
RA By P.L., Mayrhofer G.;
RT "Two genes encoding homologous 70-kDa surface proteins are present
within individual trophozoites of the binucleate protozoan parasite
Giardia intestinalis.";
RL Gene 129:257-262(1993).
CC -!- SURCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ANCHORED TO THE
PLASMA MEMBRANE.
CC -!- DOMAIN: CONTAINS 29 REPEATS OF THE CXXC MOTIF.
CC -!- SIMILARITY: BELONGS TO THE GIARDIA VARIANT SURFACE PROTEIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
CC EMBL; M33641; AAA02688.1; -;
CC EMBL; M97488; AAA02581.1; -;
CC PIR; A35502; A35502.
CC InterPro; IPR000561; EGF-like.
CC InterPro; IPR002174; Furin-like.
CC InterPro; IPR005127; Giardia_VSP.
CC Pfam; PF03302; VSP; 2.
CC SMART; SM00181; EGF; 1.
CC SMART; SM00001; EGF-like; 1.
CC SMART; SM00261; FU; 3.
CC Signal; Antigen; Glycoprotein; Transmembrane; Repeat.
FT SIGNAL 1 17
FT CHAIN 18 713 MAJOR SURFACE-LABELLED TROPHOZOITE

Thu Feb 20 11:30:52 2003

us-09-497-967-6.rsp

```
FT DOMAIN 18 679 ANTIGEN 417.
FT TRANSMEM 680 708 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 709 713 POTENTIAL.
FT CARBOHYD 289 713 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 289 713 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 676 676 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 582 582 A -> T (IN STRAIN ADELAIDE-1).
FT VARIANT 606 606 A -> S (IN STRAIN ADELAIDE-1).
FT SEQUENCE 713 AA; 72510 MW; 9AD7195843DE5601 CRC64;

Query Match 9.18; Score 213.5; DB 1; Length 713;
Best Local Similarity 23.08; Pred. No. 1.3e-07;
Matches 127; Conservative 42; Mismatches 187; Indels 197; Gaps 31;

QY 42 GTCVNCRNFFNYNGAAQ-----GEANGNQPFANNAARGI--CVPCQINRVSVTN 91
Db 111 GVCTEAAGYFAPVGAANTQSVIACGDTTGTIAAGNTYKGIADCAECSAPDATAGAE 170
QY 92 AGDLATLATQC-----STQCPTGT-----ALDD-----GV- 116
Db 171 AGKVAT-CTKGVSKYLDNVCVDAQCNSGSTNKFVAVDDSENGNKCVCSDNLNGGVA 229
QY 117 ---TDVEDRSA--ACVCCKKNFY-----NGSPQGE-APGVQVFAAG 154
Db 230 NDCYSDYDEQSKIKCTKTDNNYLKT"SEGTSCVQKQCKDGFPPKDDSSAGNKCULPCN 289
QY 155 AAAAGVAAVTSCVPCQLNKNDSPA-----TAGAQLAT-----QC 191
Db 290 DSTDGLA----NCATCALVSGRGAALVCSACTDGYKPSADKTTCEAVSNCKTPGCKAC 345
QY 192 SNQCPTGTLD--DGVTLVNTSAYL-----SKTKSAGTA---SDCTECPGKALRYGDDG 455
Db 346 SNEGKENEVCTCDGSGTYLTPISQIDSCAKIGNYYGATEGAKKLKCEKTAANCKTCDQ 405
QY 216 --CVKCRPNFYNGG--SPQGEAPGVQVFAAGAAAGVAAVTSCVPCQIHK-----NDS 266
Db 406 GQCOACNDFYKNGDACSPCHE-----SKTKSAGTA---SDCTECPGKALRYGDDG 455
QY 267 P-----ATAGAQLATQCS-----TOCPTGTAI-QDGV-----TLVFSNS 301
Db 456 TKGTCEGGCTGTGAGACKTCGLTIDGASYCECATTEYPONGVAPKASRAIPTCND 515
QY 302 STQ---CSQCIANYF-FNGN-FEA-----GKSQCLKCPVSKTTPAHAPNTATQCLIT 352
Db 516 PIQNGVCGTCADNYFRMNGGCVETVYKPGKTVCIISAPNGGTGCKAADGYKLDSGT--LT 573
QY 353 CPAGTVLDDGTSTNFVASATECTKCSAGFF--ASKTTGTAGTDTCTECKRLTSGATAK 410
Db 574 CSEG-----CKEASSTDTCTCLDGYVKSASACTKCDASCEFCNGCAATTCACATG- 624
QY 411 VYAEATOKVOCAS 423
Db 625 YYKTASGEGACTS 637

RESULT 2
LMA5_MOUSE STANDARD; PRT; 3718 AA.
AC 061001; 09JHQ6;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Laminin alpha-5 chain precursor.
GN LMA5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN RP SEQUENCE OF 1-92 FROM N.A.
RA Timpl R., Sasaki T.;
RT "Completion of the N-terminal sequence of the murine Laminin alpha 5
chain.";
```

```
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
[2]
SEQUENCE OF 84-3718 FROM N.A.
STRAIN=CS7BL/6 X CBA; TISSUE=Lung;
MEDLINE=96081906; PubMed=7499364;
Miner J.H., Lewis R.M., Sanes J.R.;
"Molecular cloning of a novel laminin chain, alpha 5, and widespread
expression in adult mouse tissues.";
J. Biol. Chem. 270:28523-28526(1995).
[3]
REVISIONS.
Miner J.H., Lewis R.M., Sanes J.R.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
is thought to mediate the attachment, migration, and organization
of cells into tissues during embryonic development by interacting
with other extracellular matrix components.
CC -!- FUNCTION: ALPHA-5 CHAIN MAY BE THE MAJOR LAMININ ALPHA CHAIN OF
ADULT EPITHELIAL AND/OR ENDOTHELIAL BASAL LAMINAE.
CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
different polypeptide chains (alpha, beta, gamma), which are bound
to each other by disulfide bonds into a cross-shaped molecule
comprising one long and three short arms with globules at each
end.
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT
MEMBRANES (MAJOR COMPONENT).
CC -!- TISSUE SPECIFICITY: IN ADULT, HIGH LEVELS IN HEART, LUNG, AND
KIDNEY; LOWER IN BRAIN, MUSCLE AND TESTIS; VERY LOW IN LIVER, GUT
AND SKIN. EXPRESSED IN MANY TISSUES IN EMBRYONIC DAY 11.
CC -!- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC -!- DOMAIN: DOMAINS VI, IV AND G ARE GLOBULAR.
CC -!- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
CC -!- SIMILARITY: CONTAINS 21.5 LAMININ EGF-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.
CC -!- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
CC
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
EMBL; AJ293593; CAB99255.1; --
EMBL; U37501; AAC53430.1; --
HSP; P02468; LTLE.
MGD; MGI:105382; Lama5.
InterPro: IPR000561; EGF-like.
InterPro: IPR001886; LamNT.
InterPro: IPR000034; Laminin_B.
InterPro: IPR002049; Laminin_EGF.
InterPro: IPR001791; Laminin_G.
Pfam; PF00052; laminin_B; 1.
Pfam; PF00053; laminin_EGF; 19.
Pfam; PF00054; laminin_G; 2.
Pfam; PF00055; laminin_Nterm; 1.
ProDom; PD002082; LamNT; 1.
ProDom; PD003031; Laminin_B; 1.
PROSITE; PS00022; EGF_1; 19.
PROSITE; PS01186; EGF_2; 3.
PROSITE; PS01248; LAMININ_TYPE_EGF; 19.
PROSITE; PS00025; LAM_G_DOMAIN; 5.
Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
SIGNAL 1 40 POTENTIAL.
CHAIN 41 3718 LAMININ ALPHA-5 CHAIN
DOMAIN 41 304 LAMININ N-TERMINAL (DOMAIN VI).
DOMAIN 305 363 LAMININ EGF-LIKE 1.
DOMAIN 364 433 LAMININ EGF-LIKE 2.
DOMAIN 434 479 LAMININ EGF-LIKE 3.
DOMAIN 500 546 LAMININ EGF-LIKE 4.
```

```
FT DOMAIN 547 592 LAMININ EGF-LIKE 5. BY SIMILARITY. 1582 1594
FT DOMAIN 593 637 LAMININ EGF-LIKE 6. DISULFID 1584 1601
FT DOMAIN 638 682 LAMININ EGF-LIKE 7. DISULFID 1584 1601
FT DOMAIN 683 728 LAMININ EGF-LIKE 8. DISULFID 1603 1612
FT DOMAIN 729 781 LAMININ EGF-LIKE 9. DISULFID 1615 1630
FT DOMAIN 782 833 LAMININ EGF-LIKE 10. DISULFID 1667 1874
FT DOMAIN 834 855 LAMININ EGF-LIKE 11 (INCOMPLETE). DISULFID 1884 1893
FT DOMAIN 856 1442 LAMININ DOMAIN IV 1 (DOMAIN IV B). DISULFID 1896 1912
FT DOMAIN 1443 1488 LAMININ EGF-LIKE 12. DISULFID 1915 1930
FT DOMAIN 1489 1532 LAMININ EGF-LIKE 13. DISULFID 1917 1939
FT DOMAIN 1533 1581 LAMININ EGF-LIKE 14. DISULFID 1941 1950
FT DOMAIN 1582 1632 LAMININ EGF-LIKE 15. DISULFID 1953 1968
FT DOMAIN 1633 1642 LAMININ EGF-LIKE 16 (N-TERMINAL). DISULFID 1971 1986
FT DOMAIN 1643 1831 LAMININ DOMAIN IV 2 (DOMAIN IV A). DISULFID 1973 1993
FT DOMAIN 1832 1864 LAMININ EGF-LIKE 17 (C-TERMINAL). DISULFID 1996 2005
FT DOMAIN 1865 1914 LAMININ EGF-LIKE 18. DISULFID 2008 2022
FT DOMAIN 1915 1970 LAMININ EGF-LIKE 19. DISULFID 2072 2083
FT DOMAIN 1971 2024 LAMININ EGF-LIKE 20. DISULFID 2074 2090
FT DOMAIN 2025 2071 LAMININ EGF-LIKE 21. DISULFID 2092 2101
FT DOMAIN 2072 2118 LAMININ EGF-LIKE 22. DISULFID 2104 2116
FT DOMAIN 2119 2168 LAMININ EGF-LIKE 23. DISULFID 2119 2126
FT DOMAIN 2169 2735 LAMININ II AND I. DISULFID 2121 2133
FT DOMAIN 2736 2933 LAMININ G-LIKE 1. DISULFID 2135 2144
FT DOMAIN 2947 3119 LAMININ G-LIKE 2. DISULFID 2147 2166
FT DOMAIN 3128 3296 LAMININ G-LIKE 3. DISULFID 2169 2172
FT DOMAIN 3337 3511 LAMININ G-LIKE 4. DISULFID 2172 2172
FT DOMAIN 3518 3689 LAMININ G-LIKE 5. CARBOHYD 100 100
FT DOMAIN 2205 2257 COILED COIL (POTENTIAL). CARBOHYD 148 148
FT DOMAIN 2330 2464 COILED COIL (POTENTIAL). CARBOHYD 248 248
FT DOMAIN 2604 2621 COILED COIL (POTENTIAL). CARBOHYD 383 383
FT DOMAIN 2639 2705 COILED COIL (POTENTIAL). CARBOHYD 457 457
FT SITE 1723 1725 CELL ATTACHMENT SITE (POTENTIAL). CARBOHYD 485 485
FT SITE 1839 1841 CELL ATTACHMENT SITE (POTENTIAL). CARBOHYD 905 905
FT DISULFID 305 314 BY SIMILARITY. CARBOHYD 926 926
FT DISULFID 307 327 BY SIMILARITY. CARBOHYD 964 964
FT DISULFID 329 338 BY SIMILARITY. CARBOHYD 964 964
FT DISULFID 341 361 BY SIMILARITY. CARBOHYD 1335 1335
FT DISULFID 364 373 BY SIMILARITY. CARBOHYD 1534 1534
FT DISULFID 366 398 BY SIMILARITY. CARBOHYD 2021 2021
FT DISULFID 401 410 BY SIMILARITY.
FT DISULFID 413 431 BY SIMILARITY.
FT DISULFID 434 445 BY SIMILARITY.
FT DISULFID 436 442 BY SIMILARITY.
FT DISULFID 454 463 BY SIMILARITY.
FT DISULFID 466 476 BY SIMILARITY.
FT DISULFID 500 512 BY SIMILARITY.
FT DISULFID 502 532 BY SIMILARITY.
FT DISULFID 535 544 BY SIMILARITY.
FT DISULFID 547 559 BY SIMILARITY.
FT DISULFID 549 566 BY SIMILARITY.
FT DISULFID 568 577 BY SIMILARITY.
FT DISULFID 580 590 BY SIMILARITY.
FT DISULFID 593 605 BY SIMILARITY.
FT DISULFID 595 611 BY SIMILARITY.
FT DISULFID 613 622 BY SIMILARITY.
FT DISULFID 625 635 BY SIMILARITY.
FT DISULFID 638 650 BY SIMILARITY.
FT DISULFID 640 656 BY SIMILARITY.
FT DISULFID 658 667 BY SIMILARITY.
FT DISULFID 670 680 BY SIMILARITY.
FT DISULFID 683 695 BY SIMILARITY.
FT DISULFID 695 702 BY SIMILARITY.
FT DISULFID 704 713 BY SIMILARITY.
FT DISULFID 716 726 BY SIMILARITY.
FT DISULFID 1443 1455 BY SIMILARITY.
FT DISULFID 1445 1462 BY SIMILARITY.
FT DISULFID 1464 1473 BY SIMILARITY.
FT DISULFID 1476 1486 BY SIMILARITY.
FT DISULFID 1533 1548 BY SIMILARITY.
FT DISULFID 1535 1555 BY SIMILARITY.
FT DISULFID 1557 1566 BY SIMILARITY.
FT DISULFID 1569 1579 BY SIMILARITY.

Query Match 8.6%; Score 202.5; DB 1; Length 3718;
Best Local Similarity 20.0%; Pred. No. 3.4e-06;
Matches 94; Conservative 36; Mismatches 150; Indels 191; Gaps 21;

QY 43 TCVNCRPNY-----YNGGAAQGEANGNQPFANNAARGICVPCQINRVGSVTN----- 91
Db 1842 SCQECAPGYRDTKGLFGRVPCQCHGHSRCLPGS--GICVGCQHTGEGDCERCPRG 1899

QY 92 --AGDLATATOC-STQCP-----TGATLDGVTDFDR-----SAAQCVKCKPNFY 136
Db 1900 FVSSDFSNFASPCVPCPLAVPSNFFADGCVLRNGRTQCLCRPGYAGASCERCAPGFF- 1958

QY 137 NGGSPQGEAPGVQVFAAGAAAAGVAATVSCVPCOLNKNDSPATAGAAANLATQCSNOCP 196
Db 1959 --GNP-----LVLGSSQPCDCSNGSDPNMIFSDCDPLTGACRGC- 1996

QY 197 TGTVLDDGTVLVNYSATLCVKCRPNFYNGGSPQGEAPGVQVFAAGAAAAGVAATVSC 256
Db 1997 -----LRHTTGPHCERCAPGY-----GNALLPGNC 2022

QY 257 VPCQINKNDSPATAGAAANLATQCSQCTGTAIOT-----GVTLVFSNHSQCS 306
Db 2023 TRC-----DCS---PCGTETCDPSGRCLKAGVT-----GORCD 2054

QY 307 QCIANFYFNGNFEACKSQCLKC-----PVSKTTPAH-----APGNTATQATQCL-- 350
Db 2055 RLEGYF-----GFECQCGCRPCACGPAKSGECPHQSQCHQCPGTTGPOCLECAPG 2107

QY 351 -----TTCPAGTVLDDGTSNFINVASATECKCSAGF---F 382
Db 2108 YWGLEKGCRCRCQPRGHCDPHTGHCTCPPG-----LSGERCDTCSQQHQVY 2155

QY 383 ASKTTGTAGTDTCTECTKKL-----TSGATAKYVAAEATOKVQCASTTEAK 428
```

Db 2156 PKPGHGHIHCEVDCHECVLLDDLERAGALLPAIREQLGINASSAAWAR 2206

RESULT 3

```

LMAL_MOUSE
ID  LMAL_MOUSE      STANDARD;      PRT;      3084 AA.
AC  P19137;
DT  01-NOV-1990 (Rel. 16, Created)
DT  01-NOV-1990 (Rel. 16, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Laminin alpha-1 chain precursor (Laminin A chain).
GN  LMAL1 OR LAMA-1 OR LAMA.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RN  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX  MEDLINE=89034134; PubMed=3182802;
RA  Sasaki M., Kleinman H.K., Huber H., Deutzmann R., Yamada Y.;
RT  "Laminin, a multidomain protein. The A chain has a unique globular
RT  domain and homology with the basement membrane proteoglycan and the
RT  laminin B chains.";
RL  J. Biol. Chem. 263:16536-16544(1988).
RN  [2]
RN  SEQUENCE OF 1-339 FROM N.A.
RX  MEDLINE=86225080; PubMed=3267223;
RA  Hartl L., Oberbaumer I., Deutzmann R.;
RT  "The N terminus of laminin A chain is homologous to the B chains.";
RL  Eur. J. Biochem. 173:629-635(1988).
RN  [3]
RN  SEQUENCE OF 2538-3084 FROM N.A., AND PARTIAL SEQUENCE.
RX  MEDLINE=89030693; PubMed=3181157;
RA  Deutzmann R., Huber J., Schmetz K.A., Oberbaumer I., Hartl L.;
RT  "Structural study of long arm fragments of laminin. Evidence for
RT  repetitive C-terminal sequences in the A-chain, not present in the B-
RT  chains.";
RL  Eur. J. Biochem. 177:35-45(1988).
CC  -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC  is thought to mediate the attachment, migration, and organization
CC  of cells into tissues during embryonic development by interacting
CC  with other extracellular matrix components.
CC  -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC  different polypeptide chains (alpha, beta, gamma), which are bound
CC  to each other by disulfide bonds into a cross-shaped molecule
CC  comprising one long and three short arms with globules at each
CC  end.
CC  THE ALPHA-1 CHAIN IS A SUBUNIT OF LAMININ-1 (EHS LAMININ) AND
CC  LAMININ-3 (S-LAMININ).
CC  -!- SUBCELLULAR LOCATION: Extracellular.
CC  -!- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
CC  COMPONENT).
CC  -!- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
CC  WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC  -!- DOMAIN: DOMAINS VI, IV AND G ARE GLOBULAR.
CC  -!- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
CC  -!- SIMILARITY: CONTAINS 17 LAMININ EGF-LIKE DOMAINS.
CC  -!- SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.
CC  -!- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
-----
CC  THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
-----
DR  EMBL; J04064; AAA39410.1; -
DR  EMBL; X07737; CAA30561.1; -
DR  EMBL; X13459; CAA31807.1; -
DR  EMBL; M36775; AAA39406.1; -
DR  PIR; A31771; MMSA.

```

```

HSSP; Q60675; IQUO.
DR  MGD; MGI:99892; Lama1.
DR  InterPro; IPR000561; EGF-like.
DR  InterPro; IPR001896; LamNT.
DR  InterPro; IPR000034; Laminin_B.
DR  InterPro; IPR002049; Laminin_EGF.
DR  InterPro; IPR001791; Laminin_G.
DR  Pfam; PF00052; laminin_B; 2.
DR  Pfam; PF00053; laminin_EGF; 15.
DR  Pfam; PF00054; laminin_G; 5.
DR  Pfam; PF00055; laminin_Nterm; 1.
DR  PRINTS; PR00011; EGF_LAMININ.
DR  PRODom; PD002082; LamNT; 1.
DR  PRODom; PD003031; Laminin_B; 2.
DR  SMART; SM00180; EGF_Lam; 14.
DR  SMART; SM00281; Lamb; 2.
DR  SMART; SM00282; LamG; 5.
DR  SMART; SM00336; LamNT; 1.
DR  PROSITE; PS00022; EGF_1; 11.
DR  PROSITE; PS01186; EGF_2; 3.
DR  PROSITE; PS01248; LAMININ_TYPE_EGF; 15.
DR  PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW  Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW  Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
FT  SIGNAL 1
FT  CHAIN 25 3084 LAMININ ALPHA-1 CHAIN.
FT  MOD_RES 25 25 BLOCKED.
FT  DOMAIN 25 276 LAMININ N-TERMINAL (DOMAIN VI).
FT  DOMAIN 277 333 LAMININ EGF-LIKE 1.
FT  DOMAIN 334 403 LAMININ EGF-LIKE 2.
FT  DOMAIN 404 460 LAMININ EGF-LIKE 3.
FT  DOMAIN 461 509 LAMININ EGF-LIKE 4.
FT  DOMAIN 510 519 LAMININ EGF-LIKE 5 (N-TERMINAL).
FT  DOMAIN 520 715 LAMININ DOMAIN IV 1 (DOMAIN IV B).
FT  DOMAIN 716 748 LAMININ EGF-LIKE 5 (C-TERMINAL).
FT  DOMAIN 749 797 LAMININ EGF-LIKE 6.
FT  DOMAIN 798 855 LAMININ EGF-LIKE 7.
FT  DOMAIN 856 908 LAMININ EGF-LIKE 8.
FT  DOMAIN 909 957 LAMININ EGF-LIKE 9.
FT  DOMAIN 958 1004 LAMININ EGF-LIKE 10.
FT  DOMAIN 1005 1050 LAMININ EGF-LIKE 11.
FT  DOMAIN 1051 1096 LAMININ EGF-LIKE 12.
FT  DOMAIN 1097 1156 LAMININ EGF-LIKE 13.
FT  DOMAIN 1157 1166 LAMININ EGF-LIKE 14 (N-TERMINAL).
FT  DOMAIN 1167 1368 LAMININ DOMAIN IV 2 (DOMAIN IV A).
FT  DOMAIN 1369 1409 LAMININ EGF-LIKE 14 (C-TERMINAL).
FT  DOMAIN 1410 1458 LAMININ EGF-LIKE 15.
FT  DOMAIN 1459 1515 LAMININ EGF-LIKE 16.
FT  DOMAIN 1516 1562 LAMININ EGF-LIKE 17.
FT  DOMAIN 1564 2124 DOMAIN II AND I.
FT  DOMAIN 2125 2305 LAMININ G-LIKE 1.
FT  DOMAIN 2313 2899 LAMININ G-LIKE 2.
FT  DOMAIN 2494 2680 LAMININ G-LIKE 3.
FT  DOMAIN 2722 2894 LAMININ G-LIKE 4.
FT  DOMAIN 2899 3079 LAMININ G-LIKE 5.
FT  DOMAIN 1612 1820 COILED COIL (POTENTIAL).
FT  DOMAIN 1869 1903 COILED COIL (POTENTIAL).
FT  DOMAIN 2096 2128 COILED COIL (POTENTIAL).
FT  SITE 1147 1149 CELL ATTACHMENT SITE.
FT  DISULFID 277 286 BY SIMILARITY.
FT  DISULFID 297 297 BY SIMILARITY.
FT  DISULFID 299 308 BY SIMILARITY.
FT  DISULFID 311 331 BY SIMILARITY.
FT  DISULFID 334 343 BY SIMILARITY.
FT  DISULFID 336 368 BY SIMILARITY.
FT  DISULFID 371 380 BY SIMILARITY.
FT  DISULFID 383 401 BY SIMILARITY.
FT  DISULFID 404 416 BY SIMILARITY.
FT  DISULFID 406 434 BY SIMILARITY.
FT  DISULFID 436 445 BY SIMILARITY.
FT  DISULFID 448 458 BY SIMILARITY.
FT  DISULFID 461 474 BY SIMILARITY.
FT  DISULFID 463 478 BY SIMILARITY.

```

FT DISULFID 480 489 BY SIMILARITY.
 FT DISULFID 492 507 BY SIMILARITY.
 FT DISULFID 749 758 BY SIMILARITY.
 FT DISULFID 751 764 BY SIMILARITY.
 FT DISULFID 767 776 BY SIMILARITY.
 FT DISULFID 779 795 BY SIMILARITY.
 FT DISULFID 798 813 BY SIMILARITY.
 FT DISULFID 800 823 BY SIMILARITY.
 FT DISULFID 826 835 BY SIMILARITY.
 FT DISULFID 838 853 BY SIMILARITY.
 FT DISULFID 856 870 BY SIMILARITY.
 FT DISULFID 858 877 BY SIMILARITY.
 FT DISULFID 880 889 BY SIMILARITY.
 FT DISULFID 892 906 BY SIMILARITY.
 FT DISULFID 909 921 BY SIMILARITY.
 FT DISULFID 911 928 BY SIMILARITY.
 FT DISULFID 930 939 BY SIMILARITY.
 FT DISULFID 942 955 BY SIMILARITY.
 FT DISULFID 958 970 BY SIMILARITY.
 FT DISULFID 960 976 BY SIMILARITY.
 FT DISULFID 978 987 BY SIMILARITY.
 FT DISULFID 990 1002 BY SIMILARITY.
 FT DISULFID 1005 1014 BY SIMILARITY.
 FT DISULFID 1007 1021 BY SIMILARITY.
 FT DISULFID 1023 1032 BY SIMILARITY.
 FT DISULFID 1035 1048 BY SIMILARITY.
 FT DISULFID 1051 1063 BY SIMILARITY.
 FT DISULFID 1053 1070 BY SIMILARITY.
 FT DISULFID 1072 1081 BY SIMILARITY.
 FT DISULFID 1084 1094 BY SIMILARITY.
 FT DISULFID 1410 1419 BY SIMILARITY.
 FT DISULFID 1412 1426 BY SIMILARITY.
 FT DISULFID 1429 1438 BY SIMILARITY.
 FT DISULFID 1441 1456 BY SIMILARITY.
 FT DISULFID 1459 1473 BY SIMILARITY.
 FT DISULFID 1461 1483 BY SIMILARITY.
 FT DISULFID 1486 1495 BY SIMILARITY.
 FT DISULFID 1498 1513 BY SIMILARITY.
 FT DISULFID 1516 1528 BY SIMILARITY.
 FT DISULFID 1518 1535 BY SIMILARITY.
 FT DISULFID 1537 1546 BY SIMILARITY.
 FT DISULFID 1549 1560 BY SIMILARITY.
 FT DISULFID 1563 1563 INTERCHAIN (PROBABLE).
 FT DISULFID 1567 1567 INTERCHAIN (PROBABLE).
 FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 370 370 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 374 374 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 531 531 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 562 562 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 770 770 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 857 857 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 914 914 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 959 959 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 969 969 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1052 1052 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1344 1344 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1414 1414 N-LINKED (GLCNAC. . .) (POTENTIAL).
 Query Match 8.5%; Score 198; DB 1; Length 3084;
 Best Local Similarity 20.0%; Pred. No. 5.8e-06;
 Matches 89; Conservative 38; Mismatches 142; Indels 176; Gaps 16;
 QY 23 CPDG-TQTQAGLTDVGAADLGTVCNCRPNFYNGGAQGEANGNPFAANNAARGICVPC 81
 DB 718 CPGGTGT-----SCEACLPYRVDGILFG-----GICQPC 749
 QY 82 QNVRGVSNTAGDLATLATQST-----QCPTG----- 109
 DB 750 ECHGHASECDTHGICSVCTHTTGDHCEQCLPGFYGTFSRGTGDCQPCACPLSIDSNFN 809
 QY 110 ---TALDGVTDVDFR-----SAAQCVKCKPNFYNGSGSPQGEAPGVQVFAAGAAAGVA 161

DB 810 SPTCHLTDGEEVVDQCAPGYSGSMCERCADGYGNTPVGG----- 851
 QY 162 AVTSQVPCQLNKNDSPATAGAQAANLATQCSNOCPTGTVLDDGVTLVFNITSATLCVKCRP 221
 DB 852 ----TCVPCNCSGNVDPLEAGHCDSDVTGEC-----LKCLWNTDGAHCERCAD 894
 QY 222 NFYYNGSGSQGEAPGVQVFAAGAAAGVAAVTSQVPCQLNKNDSPATAGAQAANLATQCS 281
 DB 895 GFY-----GDVATKNCRACDCHENG-----LS 918
 QY 282 TQCPGTGAIOGVTLVFNSTQCSQCIANYFFNGFNFEACKSQCLKCPVSKTTPAHAPGN 341
 DB 919 GVCHLETGLCDCKPHV---TGQCDQCLSGY-----GLDTGLGCVPCNCSVEGVSVD 968
 QY 342 TATQATCLTCTCPAGTVLDDGTSTNFNVASATECTKCSAGFFASKTTGTFAGTDTCTECHK 401
 DB 969 NCTEEOGC--HCGPG-----VSGKQCDRCSHGFYAFQDGG-----CTPCDC 1007
 QY 402 KLTSGATAKYAEA-----TQKVQC 421
 DB 1008 AHTQNNCDPASGECGLCPPTQGLKC 1032
 RESULT 4
 LMA2_HUMAN
 ID LMA2_HUMAN STANDARD; PRT; 3110 AA.
 AC P24043; Q14736; Q93022;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Laminin alpha-2 chain precursor (Laminin M chain) (Merosin heavy chain).
 DE chain).
 GN LAMA2 OR LAMM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_Taxid:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=94124633; PubMed=8294519;
 RA Vuolteenaho R., Missinen M., Sainio K., Byers M., Eddy R.,
 RT Hirvonen H., Shows T.B., Sariola H., Engvall E., Tryggvason K.;
 "Human laminin M chain (merosin): complete primary structure, chromosomal assignment, and expression of the M and A chain in human fetal tissues.";
 RL J. Cell Biol. 124:381-394(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97066955; PubMed=8910357;
 RA Zhang X., Vuolteenaho R., Tryggvason K.;
 RT "Structure of the human laminin alpha2-chain gene (LAMA2), which is affected in congenital muscular dystrophy.";
 RL J. Biol. Chem. 271:27664-27669(1996).
 RN [3]
 RP SEQUENCE OF 1981-3110 FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Placenta;
 RX MEDLINE=90238994; PubMed=2185464;
 RA Ehrig K., Leivo I., Argraves W.S., Ruoslahti E., Engvall E.;
 RT "Merosin, a tissue-specific basement membrane protein, is a laminin-like protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:3264-3268(1990).
 RN [4]
 RP VARIANTS GLN-545; HIS-619; LEU-919; HIS-2586 AND LYS-2614.
 RA Panicker S.G., Mendell J.T., Chen L., Feng B., Sahenk Z.,
 RT Marzluft G.A., Anato A.A., Mendell J.R.;
 RT "Novel single base polymorphisms and rare sequence variants in the laminin 2-chain coding region detected by RNA/SSCP analysis.";
 RL Hum. Mutat. 13:174-174(1999).
 RN [5]
 RP ERRATUM.
 RA Panicker S.G., Mendell J.T., Chen L., Feng B., Sahenk Z.,

RA Marzluf G.A., Amato A.A., Mendell J.R.;
RL Hum. Mutat. 13:340-340(1999).
CC -|- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration, and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -|- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end.
CC THE ALPHA-2 CHAIN IS A SUBUNIT OF LAMININ-2 (MEROSIN) AND LAMININ-
CC 4 (S-MEROSIN).
CC -|- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT
CC MEMBRANES (MAJOR COMPONENT).
CC -|- TISSUE SPECIFICITY: PLACENTA, STRIATED MUSCLE, PERIPHERAL NERVE,
CC CARDIAC MUSCLE, PANCREAS, LUNG, SPLEEN, KIDNEY, ADRENAL GLAND,
CC SKIN, TESTIS, MENINGES, CHOROID PLEXUS, AND SOME OTHER REGIONS OF
CC THE BRAIN; NOT IN LIVER, THYMUS AND BONE.
CC -|- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC -|- DOMAIN: DOMAINS VI, IV AND G ARE GLOBULAR.
CC -|- DISEASE: DEFECTS IN LAMA2 ARE THE CAUSE OF MEROSIN-DEFICIENT
CC CONGENITAL MUSCULAR DYSTROPHY (MCMC).
CC -|- SIMILARITY: CONTAINS 17 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
CC -|- SIMILARITY: CONTAINS 2 LAMININ EGF-LIKE DOMAINS.
CC -|- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>)
CC or send an email to license@isb-sib.ch).

DR EMBL; 22653; CRA81394.1; .
DR EMBL; U66796; AAB18388.1; .
DR EMBL; U66733; AAB18388.1; JOINED.
DR EMBL; U66734; AAB18388.1; JOINED.
DR EMBL; U66735; AAB18388.1; JOINED.
DR EMBL; U66736; AAB18388.1; JOINED.
DR EMBL; U66737; AAB18388.1; JOINED.
DR EMBL; U66738; AAB18388.1; JOINED.
DR EMBL; U66739; AAB18388.1; JOINED.
DR EMBL; U66740; AAB18388.1; JOINED.
DR EMBL; U66741; AAB18388.1; JOINED.
DR EMBL; U66742; AAB18388.1; JOINED.
DR EMBL; U66743; AAB18388.1; JOINED.
DR EMBL; U66745; AAB18388.1; JOINED.
DR EMBL; U66746; AAB18388.1; JOINED.
DR EMBL; U66747; AAB18388.1; JOINED.
DR EMBL; U66748; AAB18388.1; JOINED.
DR EMBL; U66749; AAB18388.1; JOINED.
DR EMBL; U66750; AAB18388.1; JOINED.
DR EMBL; U66751; AAB18388.1; JOINED.
DR EMBL; U66752; AAB18388.1; JOINED.
DR EMBL; U66753; AAB18388.1; JOINED.
DR EMBL; U66754; AAB18388.1; JOINED.
DR EMBL; U66755; AAB18388.1; JOINED.
DR EMBL; U66756; AAB18388.1; JOINED.
DR EMBL; U66757; AAB18388.1; JOINED.
DR EMBL; U66758; AAB18388.1; JOINED.
DR EMBL; U66759; AAB18388.1; JOINED.
DR EMBL; U66760; AAB18388.1; JOINED.
DR EMBL; U66761; AAB18388.1; JOINED.
DR EMBL; U66762; AAB18388.1; JOINED.
DR EMBL; U66763; AAB18388.1; JOINED.
DR EMBL; U66764; AAB18388.1; JOINED.
DR EMBL; U66765; AAB18388.1; JOINED.
DR EMBL; U66766; AAB18388.1; JOINED.
DR EMBL; U66767; AAB18388.1; JOINED.
DR EMBL; U66768; AAB18388.1; JOINED.
DR EMBL; U66769; AAB18388.1; JOINED.
DR EMBL; U66770; AAB18388.1; JOINED.
DR EMBL; U66771; AAB18388.1; JOINED.
DR EMBL; U66772; AAB18388.1; JOINED.
DR EMBL; U66773; AAB18388.1; JOINED.
DR EMBL; U66774; AAB18388.1; JOINED.
DR EMBL; U66775; AAB18388.1; JOINED.
DR EMBL; U66776; AAB18388.1; JOINED.
DR EMBL; U66777; AAB18388.1; JOINED.
DR EMBL; U66778; AAB18388.1; JOINED.
DR EMBL; U66779; AAB18388.1; JOINED.
DR EMBL; U66780; AAB18388.1; JOINED.
DR EMBL; U66781; AAB18388.1; JOINED.
DR EMBL; U66782; AAB18388.1; JOINED.
DR EMBL; U66783; AAB18388.1; JOINED.
DR EMBL; U66784; AAB18388.1; JOINED.
DR EMBL; U66785; AAB18388.1; JOINED.
DR EMBL; U66786; AAB18388.1; JOINED.
DR EMBL; U66787; AAB18388.1; JOINED.
DR EMBL; U66788; AAB18388.1; JOINED.
DR EMBL; U66789; AAB18388.1; JOINED.
DR EMBL; U66790; AAB18388.1; JOINED.
DR EMBL; U66792; AAB18388.1; JOINED.
DR EMBL; U66793; AAB18388.1; JOINED.
DR EMBL; U66794; AAB18388.1; JOINED.
DR EMBL; U66795; AAB18388.1; JOINED.
DR EMBL; M59832; AAA63215.1; .
DR PIR; A35899; MMHUMH.
DR HSP; Q60675; IQU0.
DR Genew; HGNC:6482; LAMA2.
DR MIM; 156225; .
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001886; LamNT.
DR InterPro; IPR000034; Laminin_B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR Pfam; PF00052; laminin_B; 2.
DR Pfam; PF00053; laminin_EGF; 15.
DR Pfam; PF00054; laminin_G; 5.
DR Pfam; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGF_LAMININ.
DR ProDom; PD002082; LamNT; 1.
DR ProDom; PD003031; Laminin_B; 2.
DR SMART; SM00180; EGF_Lam; 14.
DR SMART; SM00001; EGF_Like; 3.
DR SMART; SM00281; LamB; 2.
DR SMART; SM00282; LamG; 5.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00022; EGF_1; 11.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 14.
DR PROSITE; PS00025; LAM_G_DOMAIN; 5.
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal; Polymorphism.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 3110 LAMININ ALPHA-2 CHAIN.
FT DOMAIN 23 286 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 287 343 LAMININ EGF-LIKE 1.
FT DOMAIN 344 413 LAMININ EGF-LIKE 2.
FT DOMAIN 414 468 LAMININ EGF-LIKE 3.
FT DOMAIN 469 517 LAMININ EGF-LIKE 4.
FT DOMAIN 518 527 LAMININ EGF-LIKE 5 (N-TERMINAL).
FT DOMAIN 528 723 LAMININ DOMAIN IV 1 (DOMAIN IV B).
FT DOMAIN 724 756 LAMININ EGF-LIKE 5 (C-TERMINAL).
FT DOMAIN 757 806 LAMININ EGF-LIKE 6.
FT DOMAIN 807 864 LAMININ EGF-LIKE 7.
FT DOMAIN 865 917 LAMININ EGF-LIKE 8.
FT DOMAIN 918 966 LAMININ EGF-LIKE 9.
FT DOMAIN 967 1013 LAMININ EGF-LIKE 10.
FT DOMAIN 1014 1059 LAMININ EGF-LIKE 11.
FT DOMAIN 1060 1105 LAMININ EGF-LIKE 12.
FT DOMAIN 1106 1165 LAMININ EGF-LIKE 13.

```
FT DOMAIN 1166 1175 LAMININ EGF-LIKE 14 (N-TERMINAL).
FT DOMAIN 1176 1379 LAMININ DOMAIN IV 2 (DOMAIN IV A).
FT DOMAIN 1380 1419 LAMININ EGF-LIKE 14 (C-TERMINAL).
FT DOMAIN 1420 1468 LAMININ EGF-LIKE 15.
FT DOMAIN 1469 1526 LAMININ EGF-LIKE 16.
FT DOMAIN 1527 1573 LAMININ EGF-LIKE 17.
FT DOMAIN 1574 2144 DOMAIN II AND I.

Query Match 8.2%; Score 191; DB 1; Length 3110;
Best Local Similarity 24.4%; Pred. No. 1.8e-05;
Matches 113; Conservative 34; Mismatches 158; Indels 158; Gaps 30;

QY 42 GTCVNCR-----PNEYNGGAAQGEANGQFAA--NNAARICVPCQINRVG 87
DQ 771 GECLNCKDHTGGYGCYKCLPGFY--GEPTKGTSEDQPCACPLNIPSNFSTCHLDR-- 826
QY 88 SVTNAGDLATLQCSTQCTPTGTALDDGVTVDFDRSAAQVCKPKNFYNGSGQGEAPG 147
DQ 827 -----SLGLICD-GCPVG-----VTGPRCERCAEGYF--GQP--SVPG 859
QY 148 VOVFAAGAAAAGVAAVTSOCVPCOLNKNDSPATAGAAQNLATQCSNQCPTGTV----- 200
DQ 860 -----GSCQPCQCNNDLDFISPGCDLSLGSCL-ICKPGTTGRYCELC 901
QY 201 -----LDGVTLVNTSATLCVCRPNFYNGG-----SPOGEA---PGVQVFAAGAAA 246
DQ 902 ADGYFGDAV-----DAKNCQPCRCN---AGGSFSEVCHSQTGCCECRANVQGRCDKCK 952
QY 247 AGVAAVTSQ--CVPCQINKNDSPATAGAAQNLATQCSQCTPTGTATQGVTVFNSNSTQ 304
DQ 953 AGTFGLQARGCVPCNCFSGS-----KSPDCESGQC-----WCQPGVT-----GKK 995
QY 305 CSCCIANYFPNGFEAGKSCQLKCPVS-----KTPPAHAPGNT-ATQATQC----- 349
DQ 996 CDRCAHYF---NFQEG--GCTACECSHLGNNDKPKTCRCICPPNTIGERCKCAPNWTG 1050
QY 350 ---LTT---CPAGTV---LDDGTSTNF-----VASATECTKCSAGFF-----ASKTTGFT 390
DQ 1051 HSITGCKKACNSTVGSDFQCNVNTGQCNCHPKFSGAKTCESRGHWNYPKCNLCDCFL 1110
QY 391 AGTD--TCPTCKKL-----TSGATAKYAEATQKVCASITF 426
DQ 1111 PGTDATCTDSEKTKCSQDTGCTCKVNVGEIHCDCRCPKF 1153

RESULT 5
ZAN_MOUSE STANDARD; PRT; 5376 AA.
AC O88799; O08647;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Zonadhesin precursor.
GN ZAN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=98123114; PubMed=9452463;
RA Gao Z., Garbers D.L.;
RT "Species diversity in the structure of zonadhesin, a sperm-specific
RT membrane protein containing multiple cell adhesion molecule-like
RL domains.";
RL J. Biol. Chem. 273:3415-3421(1998).
RN [2]
RP SEQUENCE OF 4864-5376 FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=97271566; PubMed=9126492;
RA Gao Z., Harumi T., Garbers D.L.;
RT "Chromosome localization of the mouse zonadhesin gene and the human
```

```
RT zonadhesin gene (ZAN)";
RL Genomics 41:119-122(1997).
CC -1- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA PELLUCIDA
CC OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR
CC SIGNALING.
CC -1- SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE
CC APICAL REGION OF THE SPERM HEAD.
CC -1- TISSUE SPECIFICITY: IN TESTIS; PRIMARILY IN HAPLOID SPERMATIDS.
CC -1- DOMAIN: THE MAM DOMAINS PROBABLY MEDIATES SPERM ADHESION TO THE
CC ZONA PELLUCIDA.
CC -1- DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS,
CC THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF
CC SPERMATOZOIA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHMUS.
CC -1- DOMAIN: THE VWFD DOMAIN 2 MAY MEDIATE COVALENT
CC OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2).
CC -1- SIMILARITY: CONTAINS 3 MAM DOMAINS.
CC -1- SIMILARITY: CONTAINS 25 VWFD DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL; U97068; AAC26680.1; -
CC DR EMBL; U83190; AAC53125.1; -
CC DR MGD; MGI:106656; ZAN.
CC DR InterPro; IPR000561; EGF-like.
CC DR InterPro; IPR003645; FOLN.
CC DR InterPro; IPR000998; MAM domain.
CC DR InterPro; IPR002919; TIL_Cysrich.
CC DR InterPro; IPR003328; TILa_Cysrich.
CC DR InterPro; IPR001007; VWF_C.
CC DR InterPro; IPR001846; VWF_D.
CC DR Pfam; PF00094; vwd; 4.
CC DR Pfam; PF00629; MAM; 3.
CC DR Pfam; PF01826; TIL; 25.
CC DR Pfam; PF02345; TILa; 25.
CC DR SMART; SM00181; EGF; 2.
CC DR SMART; SM00274; FOLN; 11.
CC DR SMART; SM00137; MAM; 2.
CC DR SMART; SM00214; VWC; 17.
CC DR SMART; SM00216; VWD; 4.
CC DR PROSITE; PS00022; EGF_1; 1.
CC DR PROSITE; PS01186; EGF_2; 18.
CC DR PROSITE; PS00740; MAM_1; FALSE_NEG.
CC DR PROSITE; PS50060; MAM_2; 3.
CC KW Signal; Glycoprotein; Transmembrane; EGF-like domain; Cell adhesion;
CC Repeat.
FT SIGNAL 1 17
FT CHAIN 18 5376
FT DOMAIN 18 5310 ZONADHESIN.
FT TRANSMEM 5311 5337 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 5338 5376 POTENTIAL.
FT DOMAIN 45 210 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 215 374 MAM 1.
FT DOMAIN 377 542 MAM 2.
FT DOMAIN 547 1170 MAM 3.
FT FT 80 X HEPTAPEPTIDE REPEATS (APPROXIMATE)
FT DOMAIN 1171 1280 (MUCIN-LIKE DOMAIN).
FT DOMAIN 1281 1669 VWFD 1 (PARTIAL).
FT DOMAIN 1670 2056 VWFD 2.
FT DOMAIN 2057 2459 VWFD 3.
FT DOMAIN 2460 2579 VWFD 4.
FT DOMAIN 2580 2699 VWFD 5 (PARTIAL).
FT DOMAIN 2700 2819 VWFD 6 (PARTIAL).
FT DOMAIN 2820 2939 VWFD 7 (PARTIAL).
FT DOMAIN 2940 3059 VWFD 8 (PARTIAL).
FT DOMAIN 3060 3179 VWFD 9 (PARTIAL).
FT DOMAIN 3060 3179 VWFD 10 (PARTIAL).
```


QY 188 ATQCSN-OCPTGTVLDGVTLVFNTSATLCVK-----CRPNFYNGSGPQGE 233
Db 2671 --HCRDFOCPSGTCKD-----IKDDASNCTEIILOCPDHSLYTHCLPSCLLSCSDPDGL 2723
QY 234 APGVQVFAAGAAAGVAAVTSCQVPCQINKNDSPATAGAAQANLATQCTGPTGTATQDG 293
Db 2724 CRGTSPEAPSTCKECV-----CDPDVYVLSND-----KCVLRIECGCKDAQGVLLIPAG 2771
QY 294 VTLVFSNSTQCSQCIANVFFNGF-----EAGKSQCLKCPVSKTTPPAHAPGNT 342
Db 2772 KTWI-NRGCTQSCMGAIOCONFKEPSEAYCOYMEDGNSNCTSIPLQ--CPAH-----2823
QY 343 ATQATQCLTTC-PAGTVLD---DETSTNFVASATECTKCSAGFF-----ASK 385
Db 2824 -SHYTNCPLTCQPSCDPDGHCEGSSKTRAPSACKEGCVCEPDYVYMLNNKCVPRIECGCKD 2882
QY 386 TTGFTAGTTCCTECTKLTSGATAYAEATOKVOCASSTFEAK 428
Db 2883 TQGVLLIPADK-TWNRGCTQSCTRCGAIOCKYHCSSGTCK 2924

RESULT 6
C170_GIALA STANDARD; PRT: 328 AA.
ID C170_GIALA
AC P15799;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Surface antigen Crp170 (Fragment).
OS Giardia lamblia (Giardia intestinalis).
OC Eukaryota; Diplomonadida; Hexamitidae; Giardia.
OX NCBI_TaxID=5741;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-ATCC 30957 / WB;
RC MEDLINE=88089405; PubMed=3335828;
RA Adam R.D.; Aggarwal A.; Lal A.A.; de la Cruz V.F.; McCutchan T.;
RA Nash T.E.;
RT "Antigenic variation of a cysteine-rich protein in Giardia lamblia.";
RL J. Exp. Med. 167:109-118(1988).
CC -1- MISCELLANEOUS: CYSTEINE-RICH, ANTIGENICALLY VARIANT SURFACE
CC PROTEIN.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X06741; CAA29916.1; -
DR PIR; S00530; S00530.
DR InterPro; IPR002174; Furln-like.
DR SMART; SM00261; FU; 3.
KW Repeat; Antigen.
FT NON_TER 1 1
FT REPEAT 38 102
FT REPEAT 103 167
FT NON_TER 328 328
SQ SEQUENCE 328 AA; 33438 MW; 373A697A30EDCA21 CRC64;

Query Match 8.0%; Score 187; DB 1; Length 328;
Best Local Similarity 24.3%; Pred. No. 3.9e-06;
Matches 102; Conservative 30; Mismatches 155; Indels 132; Gaps 25;

QY 20 AVCPDGTGTQAG-LTVDGAADLTCVNCNRFNYNGSAAQGEANGNOPTAANNAARGIC 78
Db 13 AVDC-----QGSAGYTTDDSVDAKEKKC-----NAPCTACAGTADKC 51
QY 79 VPCQINRVG---SVTNAGD-LATLATQCTGCTGCTCVSAVDCQGSAGYTTDDSVSD-----AKEKKCN--- 103
Db 52 TKCDANGAARYLKKINPDPDTGTCVSAVDCQGSAGYTTDDSVSD-----AKEKKCN--- 103

FT DOMAIN 3180 3299 WVFED 11 (PARTIAL). (POTENTIAL).
FT DOMAIN 3300 3416 WVFED 12 (PARTIAL). (POTENTIAL).
FT DOMAIN 3417 3536 WVFED 13 (PARTIAL). (POTENTIAL).
FT DOMAIN 3537 3656 WVFED 14 (PARTIAL). (POTENTIAL).
FT DOMAIN 3657 3776 WVFED 15 (PARTIAL). (POTENTIAL).
FT DOMAIN 3777 3892 WVFED 16 (PARTIAL). (POTENTIAL).
FT DOMAIN 3893 4008 WVFED 17 (PARTIAL). (POTENTIAL).
FT DOMAIN 4009 4128 WVFED 18 (PARTIAL). (POTENTIAL).
FT DOMAIN 4129 4248 WVFED 19 (PARTIAL). (POTENTIAL).
FT DOMAIN 4249 4363 WVFED 20 (PARTIAL). (POTENTIAL).
FT DOMAIN 4364 4483 WVFED 21 (PARTIAL). (POTENTIAL).
FT DOMAIN 4484 4603 WVFED 22 (PARTIAL). (POTENTIAL).
FT DOMAIN 4604 4723 WVFED 23 (PARTIAL). (POTENTIAL).
FT DOMAIN 4724 4843 WVFED 24 (PARTIAL). (POTENTIAL).
FT DOMAIN 4844 5000 WVFED 25.
FT EGF-LIKE.
FT DISULFID 5263 5274 BY SIMILARITY.
FT DISULFID 5268 5283 BY SIMILARITY.
FT DISULFID 5285 5294 BY SIMILARITY.
FT CARBOHYD 339 339 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 499 499 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1216 1216 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1239 1239 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1314 1314 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1814 1814 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1908 1908 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1933 1933 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2028 2028 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2111 2111 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2142 2142 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2332 2332 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2533 2533 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2575 2575 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2692 2692 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2812 2812 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3052 3052 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3065 3065 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3144 3144 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3172 3172 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3288 3288 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3292 3292 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3782 3782 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4005 4005 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4136 4136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4243 4243 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4254 4254 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4335 4335 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4376 4376 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4586 4586 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 5136 5136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 5252 5252 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 5376 AA; 579908 MW; 0E44DB77DF2A2620 CRC64;

Query Match 8.1%; Score 189; DB 1; Length 5376;
Best Local Similarity 21.2%; Pred. No. 4e-05;
Matches 111; Conservative 56; Mismatches 204; Indels 152; Gaps 28;

QY 23 CPDGTQAGLTVGAADLTCV-----NCRPNFYNGSAAQGEANGNOPTA 69
Db 2437 CPDGTQAGLTVGAADLTCV-----NCRPNFYNGSAAQGEANGNOPTA 69
QY 70 ANNAARG-TCVP-----CQINRVGSV-----TNAG-----DLATLATQ 101
Db 2492 HSNKREGVCQGVYLRNDKCVLRIECGCQHTQGGTFIPAGKNWTSRGCSCDCMEGVIR 2551
QY 102 CST-QCPTGT---ALDDGVTDFDRSAAC-----VKCKNRYNGSGSGPGEAPGVQVF 151
Db 2552 CQNFQCPSTGYCQDIEDTGSNAC-ITLQCPAHSFTNCLPCCQPSCDPDGHCGSGSTTK 2610
QY 152 AAGAAAG-----VAAVTSQCPV-----CQ-----LNKNDSPATAGAAQANL 187
Db 2611 APSACQCGCVCEPDYVYMLNNKCVPRIECGCKDAQGVLLIPADKIWNKGTCTCACTGTI 2670

QY 135 YVNGSGPGEAPGVQVFAAGAAAGVAAVTSQVPCOLN-----KNDSPATAGAQAANLA 188
 Db 104 -----APCTACAGTA---DKCTKCDANGAAPLYLKNTPSDPTGTGCVSA 143
 QY 189 TQCSNQCPGTGVLDDGVTLVFNTSATLVCVCRPNFYVNGSGPGEAPGVQVFAAGAAAG 248
 Db 144 VDC--QGSAGYTTDSV-----SDAKECKK-----AEGOKPN-----TAG 177
 QY 249 VAAVTSQVPCQINKNKNDSPATAGAQAANLATQCSST-----QPTGT-----AIQDGYT-L 296
 Db 178 -----TQCFSC-----SDANCERCDDNDVCARCSTGAPPENGKCPAATPGCHSSCDGCTEN 238
 QY 297 VFSNSTQCSOCIANFYFNGFNFAKGS-QCL---KCPVSKTTPAHAPGNTATQATQCLTT 352
 Db 229 AMTNOADKCTGCKRGYLYKPESRAGSGACLTAECTSDKT---HFTREKAGSGKMGCLIS 285
 QY 353 CPAGTVLDDGTSNFINVASATECTKCSAGFFASKT-TGFTAGTDTCTECT-KLITSGATA 409
 Db 286 CSDAT-----HGITGCKKC-----ALKTLGSEABSTVVCSECTDKRLTPSGNA 328
 RESULT 7
 TS11_GIALA
 ID TS11_GIALA STANDARD; PRT; 667 AA.
 AC Q03185;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Major surface trophozoite antigen 11 precursor.
 GN TSPI1.
 OS Giardia lamblia (Giardia intestinalis).
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
 OX NCBI_TaxID=5741;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Isolate AD-1;
 RC MEDLINE=93241215; PubMed=8479449;
 RA Ey P.L., Khanna K., Manning P.A., Mayrhofer G.;
 RT "A gene encoding a 69-kilodalton major surface protein of Giardia
 intestinalis trophozoites";
 RL Mol. Biochem. Parasitol. 58:247-258(1993).
 CC -! SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ANCHORED TO THE
 CC PLASMA MEMBRANE.
 CC -! DOMAIN: CONTAINS 27 REPEATS OF A CXXC MOTIF.
 CC -! SIMILARITY: BELONGS TO THE GIARDIA VARIANT SURFACE PROTEIN FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M95814; AAA02687.1; -
 DR FIR; A48579; A48579.
 DR HSP; P02468; 1KLO.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR002174; Furin-like.
 DR InterPro; IPR005127; Giardia_VSP.
 DR Pfam; PF03302; VSP; 1.
 DR SMART; SM00181; EGF; 3.
 DR SMART; SM00261; FU; 5.
 DR Antigen; Repeat; Transmembrane; Signal.
 KW SIGNAL
 FT CHAIN 1 17
 FT DOMAIN 18 667 MAJOR SURFACE TROPHOZOITE ANTIGEN 11.
 FT DOMAIN 18 633 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 634 662 POTENTIAL.
 FT DOMAIN 663 667 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 591 591 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 630 630 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 667 AA; 68475 MW; 1DD95727032328BD CRC64;

Query Match 7.8%; Score 182; DB 1; Length 667;
 Best Local Similarity 22.2%; Pred No. 1.7e-05;
 Matches 120; Conservative 42; Mismatches 170; Indels 208; Gaps 32;
 QY 7 LLIISLFTNEURAVPCPDGTOT-----OAGLTDV-----GAADL-GTCVNCRPNFY 52
 Db 1 MLLAIFYFVISTITAKCTTQTQCEAEKCEMVGETEICTRCOTGKVPIDGKCVDATAN-- 58
 QY 53 YNGGAAGGANGNPPAANNAARG--ICVPCQINRVGSVT-----NAGDLATLATQC 102
 Db 59 ANCKNAGSGGDANQVCKMSSVPGNTLCITVSPDGVGSVAANEYFVPPNADATHDSVSC 118
 QY 103 STQCPFTGTDLDGVTDFDRSAAQCVKCKPNFYVNGSGPGEAPGVQVFAAGAAAGVAA 162
 Db 119 SEETPHILANNQYIGV-----AGCATC-----SAP--KAPGEDNTPRAAT----- 157
 QY 163 VTSQVPCQINKNKNDSPATAGAQAANLATQCSNOCPTGTVDLDDGVTLVFNTSAT-----LCV 217
 Db 158 ----CTKCAAGFLHTPSEG-----LSCEETCPPEG-----YFGHTATAESKKTCK 198
 QY 218 KCRPNFYVNGSGPGEAPGVQVFAAGAAAGVAAVTSQVPCQINKNKNDSPATAGAQAANLA 277
 Db 199 SC-----TGGG--SEAPNVK-----GI-----GDCLKWYNE-----ASGNTL 229
 QY 278 T--QCSTQ-----CPTGTAIQDQGVTLVFSNSTQ-- 304
 Db 230 TCEKCSAOKKPSLDKTKTSCNDCTGQNCACFCSSGGDCGCDG--FLDQGNCKVSKDCKTEN 288
 QY 305 -----CSQCIANYFFN-----GNFEAG-----KSOCLKCPVS--K 332
 Db 289 CKACTNPKAANEVTECISTHLLTPTSOCVQYCOALGNFYAGTNADNKKACKECTVANCK 348
 QY 333 T-----TPAHAPGNT--ATQATQCLTTCAGTVL---DDGISTN 366
 Db 349 TCNDQGCQTCNDGPFYKNGDACSPCHESCKTCSAGTASDC-TECTGKALAYGNDGTK-- 405
 QY 367 FVASATECTKCSAGFFASKTTGFTA-GTDTCTECTKKLTSGATAKVAEATQKVOCASSTT 425
 Db 406 --GTCGEGCTTGGSGGACKTCLTIDGASYCSECDTQ-----NEYPQNGICTSTT 453
 RESULT 8
 LMA5_HUMAN
 ID LMA5_HUMAN STANDARD; PRT; 3695 AA.
 AC O15230; Q9H1P1; Q8WZA7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Laminin alpha-5 chain precursor.
 GN LMA5 OR KIAA0533 OR KIAA1907.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Dunn N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Durr M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights K., Laird G.K., Lawlor S.,
 RA Lehasvalaho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,

FT	DISULFID	408	426	BY SIMILARITY.
FT	DISULFID	429	440	BY SIMILARITY.
FT	DISULFID	431	447	BY SIMILARITY.
FT	DISULFID	449	458	BY SIMILARITY.
FT	DISULFID	461	471	BY SIMILARITY.
FT	DISULFID	494	506	BY SIMILARITY.
FT	DISULFID	496	515	BY SIMILARITY.
FT	DISULFID	517	526	BY SIMILARITY.
FT	DISULFID	529	538	BY SIMILARITY.
FT	DISULFID	541	553	BY SIMILARITY.
FT	DISULFID	543	560	BY SIMILARITY.
FT	DISULFID	562	571	BY SIMILARITY.
FT	DISULFID	574	584	BY SIMILARITY.
FT	DISULFID	587	599	BY SIMILARITY.
FT	DISULFID	589	605	BY SIMILARITY.
FT	DISULFID	607	616	BY SIMILARITY.
FT	DISULFID	619	629	BY SIMILARITY.
FT	DISULFID	632	644	BY SIMILARITY.
FT	DISULFID	634	650	BY SIMILARITY.
FT	DISULFID	652	661	BY SIMILARITY.
FT	DISULFID	664	674	BY SIMILARITY.
FT	DISULFID	677	689	BY SIMILARITY.
FT	DISULFID	679	696	BY SIMILARITY.
FT	DISULFID	698	707	BY SIMILARITY.
FT	DISULFID	710	720	BY SIMILARITY.

Query Match

Best Local Similarity 7.8%; Score 182; DB 1; Length 3695;

Matches 97; Conservative 38; Mismatches 171; Indels 138; Gaps

QY	43	TCVNCRNPFY-----YNGGAAQGEANGNOFFAANNAARGICVPCQIN-----RVG 87
Db	1841	SCQECAPGFYRVKGLFLGRCVPCQCHGSHDRCLPGS--GVCVDQHTEGAHCERCAQ 1898
QY	88	SVTNAGDLATATQCTQCP-----TGTALDDGVTIDVDRSAAQCVCVKCPNFYNG 138
Db	1899	FVSRDDPSAPVCSC--PCPLSVPSNNFAEGCVLRGRT-----QCL-CKPG--YAG 1945
QY	139	GSPQGBAPGVQVFAAGAAAGAAVTSQVPCQLNKNDSPATAGAAQANLATQCSNQCPGT 198
Db	1946	ASCERCAPG---FFGNPLVLG-----SSCQPCDCSGNDPNLLFSDCDPLTGACRGC--- 1994
QY	199	TVLDDGVTLVFNTSATLCKVRPNFYNGSGPQGBAPGVQVFAAGAAAG-----VA 250
Db	1995	-----LRHTTGRCBICAPGYGNALLP-GNCTRCDCCTPGCTEACDPHSGHCLCKA 2044
QY	251	AVTSQ-----CVPCQINKNDSPATAGAAQAN-LATQCSQCTPGTAIQD 292
Db	2045	GVTGRRCDRCQEGHFGNCGGCRFCAC-----GPAAESECHPQSGQC--HCRPGT----- 2094
QY	293	GVTLVFSNSTQCSQCIANYFNFGNFEAGKSQLCKPCVSKTTPAHAPGNATQATQCLTT 352
Db	2095	-----NGPQCRCAPGYW--GLPEQGCRRC-QCPGGRCDP-----HTGRC--N 2132
QY	353	CPAGTVLDGDTSTNFVASATECTKCSAGF---FASKTTGTFAGTDTCTECTKKL-----T 404
Db	2133	CPFG-----LSGERCDTCSQHQHVPVPGPVGSHSIEHCEVDCVLLDLDLER 2180
QY	405	SGATAKVAEATQKVQCASTTFAX 428
Db	2181	AGALLPAIHEQLRGINASSMAWAR 2204

RESULT 9

LMA1_HUMAN

ID LMA1_HUMAN STANDARD; PRT; 3075 AA.

AC P25391;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Laminin alpha-1 chain precursor (Laminin A chain).

CN LMA1 OR LAMA.

OS Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; [1] RN SEQUENCE FROM N.A. MEDLINE=91333420; PubMed=1714537; Haaparanta T., Uitto J., Ruoslahti E., Engvall E.; "Molecular cloning of the cDNA encoding human laminin A chain."; Matrix 11:151-160(1991). [2] RN SEQUENCE OF 1-2628 FROM N.A. MEDLINE=91264789; PubMed=2049067; Nissinen M., Vuolteenaho R., Boot-Handford R., Kallunki P., Tryggvason K.; "Primary structure of the human laminin A chain. Limited expression in human tissues."; Biochem. J. 276:369-379(1991). [3] RN SEQUENCE OF 2397-3072 FROM N.A. MEDLINE=89280632; PubMed=2733383; Olsen D., Nagayoshi T., Fazio M., Peltonen J., Jaakkola S., Sanborn D., Sasaki T., Kuivaniemi H., Chu M.L., Deutzmann R., Timpl R., Uitto J.; "Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 chains, and expression of the corresponding genes in human skin and cultured cells."; Lab. Invest. 60:772-782(1989). CC -|- FUNCTION: Binding to cells via a high affinity receptor, laminin is thought to mediate the attachment, migration, and organization of cells into tissues during embryonic development by interacting with other extracellular matrix components. CC -|- SUBUNIT: Laminin is a complex glycoprotein, consisting of three different polypeptide chains (alpha, beta, gamma), which are bound to each other by disulfide bonds into a cross-shaped molecule comprising one long and three short arms with globules at each end. CC THE ALPHA-1 CHAIN IS A SUBUNIT OF LAMININ-1 (EHS LAMININ) AND LAMININ-3 (S-LAMININ). CC -|- SUBCELLULAR LOCATION: Extracellular. CC -|- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR COMPONENT). CC -|- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE. CC -|- DOMAIN: DOMAINS VI, IV AND G ARE GLOBULAR. CC -|- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI). CC -|- SIMILARITY: CONTAINS 17 LAMININ EGF-LIKE DOMAINS. CC -|- SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV. CC -|- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS. CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch). CC EMBL; X58531; CAA1418.1; -. CC PIR; S14458; S14458. CC HSSP; Q60675; LQ00. CC Genew; HGNC:6481; LAMA1. CC MIM; 150320; -. CC InterPro; IPR000561; EGF-like. CC InterPro; IPR001886; LamNT. CC InterPro; IPR000034; Laminin_B. CC InterPro; IPR002049; Laminin_G. CC Pfam; PF00052; laminin_B; 2. CC Pfam; PF00053; laminin_EGF; 15. CC Pfam; PF00054; laminin_G; 5. CC Pfam; PF00055; laminin_Nterm; 1. CC PRINTS; PR00011; EGF/LAMININ. CC ProDom; PD002082; LamNT; 1.

Query Match		7.7%	Score 181.5;	DB 1;	Length 3075;
Best Local Similarity		21.5%;	Pred. No. 7.7e-05;		
Matches	90;	Conservative	34;	Mismatches 122;	Indels 173; Gaps
24;					
QY	23	CPDP-QTQAGLTDVGAADLGTCVCNCRNFNYNGAAQG-----BANGNQPPFAANNAAR	75		: : :
Db	711	CPOGYGT-----SCSCLSGYYRVDGILFGICQPCECHG---AAECNVH	754		: : :
QY	76	GICVPQCINRVGSVTNAGDLATLATQCSTCQTCTALTDDGVDFDRSAQQVKCKPNFY	135	:	:
Db	755	GVCIACAHNTTG-----VHC EQCLPGFY	777	:	:
QY	136	YNGGSPQGEAPGVQVFPAAGAAAAGVAAVTSOCPCQLNKNDSPATAQAQANLATQCSNO	195		:
Db	778	--GEFSRGTPG-----DCQPCA-----CPLTI--ASNFSPTCH---	807		:
QY	196	PTGTVLDDGGTVLVFN-----TSATLCVKRCRNPFYNGSSPQGEAPGVQVFPAAGAAAGA	250	:	:
Db	808	----LNDGDEVVCDWCAFGYGAMCERCABGY--GNP--TVPG-----	843	:	:
QY	251	AVTSQCVPCQIINKNDSPATAQAQANLATQSTCQPTGTALIQDGVTLVFSNSQTCCSQCIA	310		:
Db	844	---ESCVPDCSGNDVPSEAGHCDSDVTGC-LKCLGNI---DG-----AHCERC-A	886		:
QY	311	NYPFNGNEAGKSQCLKCPV--SKTTPAH-----APGNATAQTQACL-----	350	:	:

[4]
X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 2932-3106.
MEDLINE=20085745; PubMed=10619025;
Hohenester E., Tisi D., Taits J.F., Timpl R.;
"The crystal structure of a laminin G-like module reveals the
molecular basis of alpha-dystroglycan binding to laminins, perlecan,
and agrin.";
Mol. Cell 4:783-792(1999).
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
is thought to mediate the attachment, migration, and organization
of cells into tissues during embryonic development by interacting
with other extracellular matrix components.
CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
different polypeptide chains (alpha, beta, gamma), which are bound
to each other by disulfide bonds into a cross-shaped molecule
Comprising one long and three short arms with globules at each
end.
CC THE ALPHA-2 CHAIN IS A SUBUNIT OF LAMININ-2 (MEROSIN) AND LAMININ-
4 (S-MEROSIN).
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
COMPONENT).
CC -!- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC -!- DOMAIN: DOMAINS VI, IV AND G ARE GLOBULAR.
CC -!- DISAID: DEFECTS IN LAMA2 ARE A CAUSE OF MURINE MUSCULAR DYSTROPHY
(DYZ2).
CC -!- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
CC -!- SIMILARITY: CONTAINS 17 LAMININ EGF-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.
CC -!- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).

EMBL; U12147; AAC52165.1; -;
EMBL; X69869; CAA49502.1; -;
EMBL; S75315; AAB33573.1; -;
PDB; 1QU0; O3-DEC-99.
MCD; MGI:99912; Lama2.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001886; LamNT.
DR InterPro; IPR000034; Laminin_B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR Pfam; PF00052; laminin_B; 2.
DR Pfam; PF00053; laminin_EGF; 15.
DR Pfam; PF00054; laminin_G; 5.
DR Pfam; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGFLAMININ.
DR ProDom; PD002082; LamNT; 1.
DR ProDom; PD03031; Laminin_B; 2.
DR SMART; SM00180; EGF_Lam; 15.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00281; Lamb; 2.
DR SMART; SM00282; Lang; 5.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00022; EGF_1; 11.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 14.
DR PROSITE; PS50025; IAM_G_DOMAIN; 5.
KW Glycoprotein. Basement membrane; Extracellular matrix; Coiled coil;
Laminin EGF-like domain; Cell adhesion; Repeat; Signal; 3D structure.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 3106 LAMININ ALPHA-2 CHAIN.
FT DOMAIN 23 282 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 283 339 LAMININ EGF-LIKE 1.
FT DOMAIN 340 409 LAMININ EGF-LIKE 2.

EMBL; X05211; CAA28838.1; -;
DR EMBL; J03484; AAA39405.1; -;
DR EMBL; J02930; AAA39408.1; -;
DR EMBL; J03749; AAA39409.1; -;
DR PIR; A28469; MMSB2.
DR PDB; 1KLO; 20-AUG-97.
DR PDB; 1LLE; 12-FEB-97.
DR MGI; 99914; Lamcl.
DR InterPro; IPR004089; Chmtaxis_transd.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001886; LamNT.
DR InterPro; IPR000034; Laminin_B.
DR InterPro; IPR002049; Laminin_EGF.
DR Pfam; PF00052; laminin_B; 1.
DR Pfam; PF00053; laminin_EGF; 10.
DR Pfam; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGF_LAMININ.
DR ProDom; PD002082; LamNT; 1.
DR ProDom; PD003031; Laminin_B; 1.
DR SMART; SM00180; EGF_Lam; 9.
DR SMART; SM00001; EGF_Like; 1.
DR SMART; SM00281; LamB; 1.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 10.
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal; 3D-structure.
FT SIGNAL 1 33
FT CHAIN 34 1607 LAMININ GAMMA-1 CHAIN.
FT DOMAIN 34 283 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 284 339 LAMININ EGF-LIKE 1.
FT DOMAIN 340 395 LAMININ EGF-LIKE 2.
FT DOMAIN 396 442 LAMININ EGF-LIKE 3.
FT DOMAIN 443 492 LAMININ EGF-LIKE 4.
FT DOMAIN 493 502 LAMININ EGF-LIKE 5 (N-TERMINAL).
FT DOMAIN 503 687 LAMININ DOMAIN IV.
FT DOMAIN 688 721 LAMININ EGF-LIKE 5 (C-TERMINAL).
FT DOMAIN 722 770 LAMININ EGF-LIKE 6.
FT DOMAIN 771 825 LAMININ EGF-LIKE 7.
FT DOMAIN 826 881 LAMININ EGF-LIKE 8 (NIDOGEM-BINDING).
FT DOMAIN 882 932 LAMININ EGF-LIKE 9.
FT DOMAIN 933 980 LAMININ EGF-LIKE 10.
FT DOMAIN 981 1028 LAMININ EGF-LIKE 11.
FT DOMAIN 1029 1607 DOMAIN II AND I.
FT DOMAIN 1034 1394 COILED COIL (POTENTIAL).
FT DISULFID 340 349 BY SIMILARITY.
FT DISULFID 342 365 BY SIMILARITY.
FT DISULFID 368 377 BY SIMILARITY.
FT DISULFID 380 393 BY SIMILARITY.
FT DISULFID 396 408 BY SIMILARITY.
FT DISULFID 398 414 BY SIMILARITY.
FT DISULFID 416 425 BY SIMILARITY.
FT DISULFID 428 440 BY SIMILARITY.
FT DISULFID 443 454 BY SIMILARITY.
FT DISULFID 445 461 BY SIMILARITY.
FT DISULFID 463 472 BY SIMILARITY.
FT DISULFID 475 490 BY SIMILARITY.
FT DISULFID 722 731 BY SIMILARITY.
FT DISULFID 724 738 BY SIMILARITY.
FT DISULFID 740 749 BY SIMILARITY.
FT DISULFID 752 768 BY SIMILARITY.
FT DISULFID 771 779 BY SIMILARITY.
FT DISULFID 773 790 BY SIMILARITY.
FT DISULFID 793 802 BY SIMILARITY.
FT DISULFID 805 823 BY SIMILARITY.
FT DISULFID 826 840 BY SIMILARITY.
FT DISULFID 828 857 BY SIMILARITY.
FT DISULFID 850 859 BY SIMILARITY.
FT DISULFID 862 879 BY SIMILARITY.
FT DISULFID 882 896 BY SIMILARITY.
FT DISULFID 884 903 BY SIMILARITY.

FT DISULFID 905 914 BY SIMILARITY.
FT DISULFID 917 930 BY SIMILARITY.
FT DISULFID 933 945 BY SIMILARITY.
FT DISULFID 935 952 BY SIMILARITY.
FT DISULFID 954 963 BY SIMILARITY.
FT DISULFID 966 978 BY SIMILARITY.
FT DISULFID 981 993 BY SIMILARITY.
FT DISULFID 983 999 BY SIMILARITY.
FT DISULFID 1001 1010 BY SIMILARITY.
FT DISULFID 1013 1026 BY SIMILARITY.
FT DISULFID 1029 1029 INTERCHAIN (PROBABLE).
FT DISULFID 1032 1032 INTERCHAIN (WITH CHAIN BETA-1).
FT DISULFID 1598 1598 INTERCHAIN (PROBABLE).
FT CARBOHYD 58 58 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 574 574 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 648 648 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1020 1020 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1105 1105 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1159 1159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1173 1173 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1203 1203 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1221 1221 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1239 1239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1378 1378 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1393 1393 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1437 1437 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 216 216 G -> A (IN REF. 3).
FT CONFLICT 260 260 E -> D (IN REF. 2).
FT CONFLICT 337 337 S -> C (IN REF. 2).
FT CONFLICT 447 448 LR -> PS (IN REF. 2).
FT CONFLICT 544 544 D -> Y (IN REF. 2).
FT CONFLICT 662 662 T -> S (IN REF. 2).
FT CONFLICT 886 886 MISSING (IN REF. 2).
FT CONFLICT 1158 1158 MISSING (IN REF. 2).
FT CONFLICT 1434 1434 V -> A (IN REF. 2).
FT CONFLICT 1475 1475 R -> K (IN REF. 4).
FT CONFLICT 1576 1576 D -> N (IN REF. 4).
SQ SEQUENCE 1607 AA; 177297 MW; 81B7B08B4E69F242 CRC64;

Query Match 7.6%; Score 177.5; DB 1; Length 1607;
Best Local Similarity 20.7%; Pred. No. 7.8e-05;
Matches 79; Conservative 35; Mismatches 127; Indels 141; Gaps 20;

QY 44 CVNCRPNFYNGAAGEANGNPFFAANNAARGICVPCQINRVGSVTNAGDLATLATQCS 103
Db 749 CEKCSGYY--GDSLTGTSSDCQPCPCGGSSCAIYP-----KKEVWC- 790
QY 104 TQPTGTALDDGYDVFDRSAACQCKPNFYNGSGPOGEAPGVQVFAAGAAAAGVAAV 163
Db 791 THCTGTGA-----GKRCELDDGYF--GDPLGNGPVL-----822
QY 164 TSQCVPCQLNKNDSPATAGAAANLATQCSNQCPGTGTVLDGVTLVFNTSATLCKVCRPNF 223
Db 823 ---CRPCCNDNIDPNVAGNCNRLTGEC-----LKCITYNTAGFYCDRCKEGF 866
QY 224 YNNGSGPQGEAPGVQVFAAGAAAAGVAAVTSQCVPCQINKNDSPATAGAAANLATQCSSTQ 283
Db 867 F---GNPLAPNPADKKKACACPNYGTVOQSSCNP-----VTGQC--Q 904
QY 284 CPTGTATODGVTLVFSNSSTQCSQCIANYFFNGFNGFEAGKSOCLKCPVSKTTPAHAPGNTA 343
Db 905 CLPHVSGRD-----CGTCDFGY--NLQSGQG-CERC-----DCHALGSTN 942
QY 344 TQAT-----QCLTTCPTAGTVLDGTVSTNFVASAETCKSAGFTASKTTGTTAGTDTCTEC 399
Db 943 GQCDIRTGQC--ECQPG-----ITGQHCERCETNHF-----GF--GPEGCKPC 981
QY 400 TKKLTSGATAKVYAETQKVC 421
Db 982 -----DCHHEGSLSLQOC 993

RESULT 13
 LMG3_HUMAN
 ID LMG3_HUMAN STANDARD; PRT; 1587 AA.
 AC Q916N6;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Laminin gamma-3 chain precursor (Laminin 12 gamma 3).
 GN LMG3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=99242614; PubMed=10225960;
 RA Koch M., Olson P.F., Albus A., Jin W., Hunter D.D., Brunken W.J.,
 RA Burgeson R.E., Champlaud M.F.;
 RT "Characterization and expression of the laminin gamma3 chain: a novel,
 RT non-basement membrane-associated, laminin chain.";
 RL J. Cell Biol. 145:605-618(1999).
 CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
 CC is thought to mediate the attachment, migration, and organization
 CC of cells into tissues during embryonic development by interacting
 CC with other extracellular matrix components.
 CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 CC different polypeptide chains (alpha, beta, gamma), which are bound
 CC to each other by disulfide bonds into a cross-shaped molecule
 CC comprising one long and three short arms with globules at each
 CC end.
 CC THE GAMMA-3 CHAIN IS A SUBUNIT OF LAMININ-12.
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- TISSUE SPECIFICITY: Broadly expressed in: skin, heart, lung, and
 CC the reproductive tracts.
 CC -!- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
 CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
 CC -!- DOMAIN: DOMAIN IV IS GLOBULAR.
 CC -!- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
 CC -!- SIMILARITY: CONTAINS 11 LAMININ EGF-LIKE DOMAINS.
 CC -!- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AF041835; AAD36991.1; -;
 CC HSSP: P02468; 1TLE.
 CC Genew: HGNC:6494; LMG3.
 CC MIM: 604349; -;
 CC InterPro: IPR000561; EGF-like.
 CC InterPro: IPR001886; LamNT.
 CC InterPro: IPR000034; Laminin_B.
 CC InterPro: IPR002049; Laminin_EGF.
 CC Pfam: PF00052; laminin_B; 1.
 CC Pfam: PF00053; laminin_EGF; 10.
 CC Pfam: PF00055; laminin_Nterm; 1.
 CC PRINTS: P00011; EGF_LAMININ.
 CC ProDom: P0002082; LamNT; 1.
 CC ProDom: P0003031; Laminin_B; 1.
 CC SMART: SM00180; EGF_Lam; 10.
 CC SMART: SM00001; EGF_Like; 1.
 CC SMART: SM00281; LamB; 1.
 CC SMART: SM00136; LamNT; 1.
 CC PROSITE: PS00022; EGF_1; 7.
 CC PROSITE: PS01186; EGF_2; 2.
 CC PROSITE: PS01248; LAMININ_TYPE_EGF; 10.
 CC Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
 KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.

FT	SIGNAL	1	19	POTENTIAL
FT	CHAIN	20	1587	LAMININ GAMMA-3 CHAIN.
FT	DOMAIN	20	270	LAMININ N-TERMINAL (DOMAIN VI).
FT	DOMAIN	271	326	LAMININ EGF-LIKE 1.
FT	DOMAIN	327	382	LAMININ EGF-LIKE 2.
FT	DOMAIN	383	429	LAMININ EGF-LIKE 3.
FT	DOMAIN	430	479	LAMININ EGF-LIKE 4.
FT	DOMAIN	480	489	LAMININ EGF-LIKE 5 (N-TERMINAL).
FT	DOMAIN	490	672	LAMININ DOMAIN IV.
FT	DOMAIN	673	706	LAMININ EGF-LIKE 5 (C-TERMINAL).
FT	DOMAIN	707	754	LAMININ EGF-LIKE 6.
FT	DOMAIN	755	809	LAMININ EGF-LIKE 7.
FT	DOMAIN	810	865	LAMININ EGF-LIKE 8.
FT	DOMAIN	866	916	LAMININ EGF-LIKE 9.
FT	DOMAIN	917	964	LAMININ EGF-LIKE 10.
FT	DOMAIN	965	1013	LAMININ EGF-LIKE 11.
FT	DOMAIN	1014	1587	DOMAIN II AND I.
FT	DOMAIN	1071	1141	COILED COIL (POTENTIAL).
FT	DOMAIN	1200	1229	COILED COIL (POTENTIAL).
FT	DOMAIN	1424	1504	COILED COIL (POTENTIAL).
FT	DOMAIN	1535	1579	COILED COIL (POTENTIAL).
FT	SITE	1059	1061	CELL ATTACHMENT SITE (POTENTIAL).
FT	CARBOHYD	87	87	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	119	119	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	295	295	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	328	328	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	631	631	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	837	837	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	980	980	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1185	1185	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1518	1518	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1587	1587	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	SEQUENCE	1587	1587	AA; 172051 MW; 3CB6E09B5F203319 CRC64;

Query Match 7.5%; Score 175; DB 1; Length 1587;
 Best Local Similarity 19.7%; Pred. No. 0.00011;
 Matches 89; Conservative 43; Mismatches 155; Indels 164; Gaps 21;

QY	13	LFTELRAVPCDGTQAGLTDVGAADLG----	TCVNCRPNFYNGGAQGEANGNOPF	68
DB	649	VFLTEVRLTSARPLSPASWVEICSCPTGYTGQFCESCAPGY-----	KREMPQGGPY	701
QY	69	AANNAARGICVPCQINRVGSVTVNAGDLATLATQCS--TCPTGTALDDGVTVDVDRSAQ	126	
DB	702	AS-----CVPTCQHQGTGTC-----DPNTGICVCSHTEGGS-	732	
QY	127	CVKCKPNFYNGGSP--QGEAPGVQVFAAGAAAA--	158	
DB	733	CERCLPGFY---GNPPAGQADDCQPCPCGQSACTIPESGEVCTHCPPQGRGRCEVC	789	
QY	159	-----GVAAVTSQCVPCQINRVGSVTVNAGDLATLATQCS--TCPTGTALDDGVTVDVDRSAQ	209	
DB	790	DGFFGFDPLGLFQHPQPCQCCSGNVDPNAVGNCDPLSGHC-----	LRCLH	
QY	210	NTSATLCVKCRPNFYNGGSPQGEAPGVQVFAAGAAAAVAVTSQCVPCQINRVGSVTVNAGDLATLATQCS--TCPTGTALDDGVTVDVDRSAQ	269	
DB	837	NTGDCHEHCQGGFY---GSALAPRP-----ADKCMPCSCHPQGSVSE	876	
QY	270	ACAQANLATQCSCTQCTGTCTAIGDVTLVFNSNSTQCSQCIANYFNGFNGFAGKSOCLKCP	329	
DB	877	QMPCDPVTGQCS--CLPHVTARD-----CSRCPGFF--DLQPERG-CRSC-	917	
QY	330	VSKTTPAHAPGNTATQ-----ATQCLTTCAGTVDLDDGTTSTNFVASATECTKCSAGFFASK	385	
DB	918	-----KCHPLGSDQEDQCHPKTQC--TCRPG-----VTGQACDRCLQGLFGFS	958	
QY	386	TTGFTAGTDTCTECTKLTLSGATKVAEAT	416	
DB	959	IKG-----CRACRCSPLGAASQACHYNGT	982	

RESULT 14
 LMB1_DROME
 ID LMB1_DROME STANDARD; PRT; 1790 AA.

Thu Feb 20 11:30:52 2003

AC P11046; Q26328; Q9XZT4; Q9VLM6;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Laminin beta-1 chain precursor (Laminin B1 chain).
 GN LAMB1 OR LAMB1 OR C7123.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 CC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Canton-S;
 RX MEDLINE=94000382; PubMed=8397815;
 RA Gow C.-H., Chang H.-Y., Lih C.-J., Chang T.-W., Hui C.-F.;
 FT "Analysis of the Drosophila gene for the laminin B1 chain.";
 RL DNA Cell Biol. 12:573-587(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88210471; PubMed=3365769;
 RA Montell D.J., Goodman C.S.;
 RT "Drosophila substrate adhesion molecule: sequence of laminin B1 chain
 reveals domains of homology with mouse.";
 RL Cell 53:463-473(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
 RA George R.A., Lewis S.E., Yandell M.D., Zhang Q., Chen L.X.,
 RA Sutton G.G., Wortman J.R., Binkley J., Davis R., Olsen K.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt J.G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Drenth J., Dew I., Dietz S.M.,
 RA Dodson J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
 is thought to mediate the attachment, migration, and organization
 of cells into tissues during embryonic development by interacting
 with other extracellular matrix components.
 CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 different polypeptide chains (alpha, beta, gamma), which are bound

to each other by disulfide bonds into a cross-shaped molecule
 Comprising one long and three short arms with globules at each
 end.
 -1- SUBCELLULAR LOCATION: Extracellular.
 -1- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
 COMPONENT).
 -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
 WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
 -1- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.
 -1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
 -1- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.
 -1- SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

 CC EMBL; M95811; AAD19752.1; -;
 CC EMBL; M19525; AAA28663.1; -;
 CC EMBL; AE003618; AAF52563.1; -;
 CC PIR; A28783; MMFFBI.
 CC HSSP; P02468; ITLE.
 CC FlyBase; FBgn0002527; LaminB1.
 CC InterPro; IPR000561; EGF-like.
 CC InterPro; IPR001886; LaminT.
 CC InterPro; IPR002049; Laminin_EGF.
 CC Pfam; PF00053; laminin_EGF; 13.
 CC PRINTS; PR00011; EGF_LAMININ.
 CC ProDom; PD002082; LaminT; 1.
 CC SMART; SM00180; EGF_Lam; 11.
 CC SMART; SM00001; EGF_Like; 1.
 CC SMART; SM00136; LaminT; 1.
 CC PROSITE; PS00022; EGF_1; 10.
 CC PROSITE; PS00186; EGF_2; 2.
 CC PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
 CC GlycoProtein; Basement membrane; Extracellular matrix; Coiled coil;
 KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
 FT SIGNAL 1 25
 FT CHAIN 26 1790 LAMININ BETA-1 CHAIN.
 FT DOMAIN 43 289 LAMININ N-TERMINAL (DOMAIN VI).
 FT DOMAIN 290 356 LAMININ EGF-LIKE 1.
 FT DOMAIN 357 419 LAMININ EGF-LIKE 2.
 FT DOMAIN 420 479 LAMININ EGF-LIKE 3.
 FT DOMAIN 480 530 LAMININ EGF-LIKE 4.
 FT DOMAIN 531 561 LAMININ EGF-LIKE 5 (INCOMPLETE).
 FT DOMAIN 562 789 LAMININ DOMAIN IV.
 FT DOMAIN 791 838 LAMININ EGF-LIKE 6.
 FT DOMAIN 839 884 LAMININ EGF-LIKE 7.
 FT DOMAIN 885 934 LAMININ EGF-LIKE 8.
 FT DOMAIN 935 992 LAMININ EGF-LIKE 9.
 FT DOMAIN 993 1044 LAMININ EGF-LIKE 10.
 FT DOMAIN 1045 1095 LAMININ EGF-LIKE 11.
 FT DOMAIN 1096 1143 LAMININ EGF-LIKE 12.
 FT DOMAIN 1144 1190 LAMININ EGF-LIKE 13.
 FT DOMAIN 1191 1407 DOMAIN II.
 FT DOMAIN 1408 1434 DOMAIN ALPHA.
 FT DOMAIN 1435 1790 DOMAIN I.
 FT DOMAIN 1791 1807 COILED COIL (POTENTIAL).
 FT DOMAIN 1808 1824 COILED COIL (POTENTIAL).
 FT DOMAIN 1825 1841 COILED COIL (POTENTIAL).
 FT DOMAIN 1842 1858 COILED COIL (POTENTIAL).
 FT DOMAIN 1859 1875 BY SIMILARITY.
 FT DOMAIN 1876 1892 BY SIMILARITY.
 FT DOMAIN 1893 1909 BY SIMILARITY.
 FT DOMAIN 1910 1926 BY SIMILARITY.
 FT DOMAIN 1927 1943 BY SIMILARITY.
 FT DOMAIN 1944 1960 BY SIMILARITY.
 FT DOMAIN 1961 1977 BY SIMILARITY.
 FT DOMAIN 1978 1994 BY SIMILARITY.
 FT DOMAIN 1995 2011 BY SIMILARITY.
 FT DOMAIN 2012 2028 BY SIMILARITY.
 FT DOMAIN 2029 2045 BY SIMILARITY.
 FT DOMAIN 2046 2062 BY SIMILARITY.
 FT DOMAIN 2063 2079 BY SIMILARITY.
 FT DOMAIN 2080 2096 BY SIMILARITY.
 FT DOMAIN 2097 2113 BY SIMILARITY.
 FT DOMAIN 2114 2130 BY SIMILARITY.
 FT DOMAIN 2131 2147 BY SIMILARITY.
 FT DOMAIN 2148 2164 BY SIMILARITY.
 FT DOMAIN 2165 2181 BY SIMILARITY.
 FT DOMAIN 2182 2198 BY SIMILARITY.
 FT DOMAIN 2199 2215 BY SIMILARITY.
 FT DOMAIN 2216 2232 BY SIMILARITY.
 FT DOMAIN 2233 2249 BY SIMILARITY.
 FT DOMAIN 2250 2266 BY SIMILARITY.
 FT DOMAIN 2267 2283 BY SIMILARITY.
 FT DOMAIN 2284 2300 BY SIMILARITY.
 FT DOMAIN 2301 2317 BY SIMILARITY.
 FT DOMAIN 2318 2334 BY SIMILARITY.
 FT DOMAIN 2335 2351 BY SIMILARITY.
 FT DOMAIN 2352 2368 BY SIMILARITY.
 FT DOMAIN 2369 2385 BY SIMILARITY.
 FT DOMAIN 2386 2402 BY SIMILARITY.
 FT DOMAIN 2403 2419 BY SIMILARITY.
 FT DOMAIN 2420 2436 BY SIMILARITY.
 FT DOMAIN 2437 2453 BY SIMILARITY.
 FT DOMAIN 2454 2470 BY SIMILARITY.
 FT DOMAIN 2471 2487 BY SIMILARITY.
 FT DOMAIN 2488 2504 BY SIMILARITY.
 FT DOMAIN 2505 2521 BY SIMILARITY.
 FT DOMAIN 2522 2538 BY SIMILARITY.
 FT DOMAIN 2539 2555 BY SIMILARITY.
 FT DOMAIN 2556 2572 BY SIMILARITY.
 FT DOMAIN 2573 2589 BY SIMILARITY.
 FT DOMAIN 2590 2606 BY SIMILARITY.
 FT DOMAIN 2607 2623 BY SIMILARITY.
 FT DOMAIN 2624 2640 BY SIMILARITY.
 FT DOMAIN 2641 2657 BY SIMILARITY.
 FT DOMAIN 2658 2674 BY SIMILARITY.
 FT DOMAIN 2675 2691 BY SIMILARITY.
 FT DOMAIN 2692 2708 BY SIMILARITY.
 FT DOMAIN 2709 2725 BY SIMILARITY.
 FT DOMAIN 2726 2742 BY SIMILARITY.
 FT DOMAIN 2743 2759 BY SIMILARITY.
 FT DOMAIN 2760 2776 BY SIMILARITY.
 FT DOMAIN 2777 2793 BY SIMILARITY.
 FT DOMAIN 2794 2810 BY SIMILARITY.
 FT DOMAIN 2811 2827 BY SIMILARITY.
 FT DOMAIN 2828 2844 BY SIMILARITY.
 FT DOMAIN 2845 2861 BY SIMILARITY.
 FT DOMAIN 2862 2878 BY SIMILARITY.
 FT DOMAIN 2879 2895 BY SIMILARITY.
 FT DOMAIN 2896 2912 BY SIMILARITY.
 FT DOMAIN 2913 2929 BY SIMILARITY.
 FT DOMAIN 2930 2946 BY SIMILARITY.
 FT DOMAIN 2947 2963 BY SIMILARITY.
 FT DOMAIN 2964 2980 BY SIMILARITY.
 FT DOMAIN 2981 2997 BY SIMILARITY.
 FT DOMAIN 2998 3014 BY SIMILARITY.
 FT DOMAIN 3015 3031 BY SIMILARITY.
 FT DOMAIN 3032 3048 BY SIMILARITY.
 FT DOMAIN 3049 3065 BY SIMILARITY.
 FT DOMAIN 3066 3082 BY SIMILARITY.
 FT DOMAIN 3083 3099 BY SIMILARITY.
 FT DOMAIN 3100 3116 BY SIMILARITY.
 FT DOMAIN 3117 3133 BY SIMILARITY.
 FT DOMAIN 3134 3150 BY SIMILARITY.
 FT DOMAIN 3151 3167 BY SIMILARITY.
 FT DOMAIN 3168 3184 BY SIMILARITY.
 FT DOMAIN 3185 3201 BY SIMILARITY.
 FT DOMAIN 3202 3218 BY SIMILARITY.
 FT DOMAIN 3219 3235 BY SIMILARITY.
 FT DOMAIN 3236 3252 BY SIMILARITY.
 FT DOMAIN 3253 3269 BY SIMILARITY.
 FT DOMAIN 3270 3286 BY SIMILARITY.
 FT DOMAIN 3287 3303 BY SIMILARITY.
 FT DOMAIN 3304 3320 BY SIMILARITY.
 FT DOMAIN 3321 3337 BY SIMILARITY.
 FT DOMAIN 3338 3354 BY SIMILARITY.
 FT DOMAIN 3355 3371 BY SIMILARITY.
 FT DOMAIN 3372 3388 BY SIMILARITY.
 FT DOMAIN 3389 3405 BY SIMILARITY.
 FT DOMAIN 3406 3422 BY SIMILARITY.
 FT DOMAIN 3423 3439 BY SIMILARITY.
 FT DOMAIN 3440 3456 BY SIMILARITY.
 FT DOMAIN 3457 3473 BY SIMILARITY.
 FT DOMAIN 3474 3490 BY SIMILARITY.
 FT DOMAIN 3491 3507 BY SIMILARITY.
 FT DOMAIN 3508 3524 BY SIMILARITY.
 FT DOMAIN 3525 3541 BY SIMILARITY.
 FT DOMAIN 3542 3558 BY SIMILARITY.
 FT DOMAIN 3559 3575 BY SIMILARITY.
 FT DOMAIN 3576 3592 BY SIMILARITY.
 FT DOMAIN 3593 3609 BY SIMILARITY.
 FT DOMAIN 3610 3626 BY SIMILARITY.
 FT DOMAIN 3627 3643 BY SIMILARITY.
 FT DOMAIN 3644 3660 BY SIMILARITY.
 FT DOMAIN 3661 3677 BY SIMILARITY.
 FT DOMAIN 3678 3694 BY SIMILARITY.
 FT DOMAIN 3695 3711 BY SIMILARITY.
 FT DOMAIN 3712 3728 BY SIMILARITY.
 FT DOMAIN 3729 3745 BY SIMILARITY.
 FT DOMAIN 3746 3762 BY SIMILARITY.
 FT DOMAIN 3763 3779 BY SIMILARITY.
 FT DOMAIN 3780 3796 BY SIMILARITY.
 FT DOMAIN 3797 3813 BY SIMILARITY.
 FT DOMAIN 3814 3830 BY SIMILARITY.
 FT DOMAIN 3831 3847 BY SIMILARITY.
 FT DOMAIN 3848 3864 BY SIMILARITY.
 FT DOMAIN 3865 3881 BY SIMILARITY.
 FT DOMAIN 3882 3898 BY SIMILARITY.
 FT DOMAIN 3899 3915 BY SIMILARITY.
 FT DOMAIN 3916 3932 BY SIMILARITY.
 FT DOMAIN 3933 3949 BY SIMILARITY.
 FT DOMAIN 3950 3966 BY SIMILARITY.
 FT DOMAIN 3967 3983 BY SIMILARITY.
 FT DOMAIN 3984 4000 BY SIMILARITY.
 FT DOMAIN 4001 4017 BY SIMILARITY.
 FT DOMAIN 4018 4034 BY SIMILARITY.
 FT DOMAIN 4035 4051 BY SIMILARITY.
 FT DOMAIN 4052 4068 BY SIMILARITY.
 FT DOMAIN 4069 4085 BY SIMILARITY.
 FT DOMAIN 4086 4102 BY SIMILARITY.
 FT DOMAIN 4103 4119 BY SIMILARITY.
 FT DOMAIN 4120 4136 BY SIMILARITY.
 FT DOMAIN 4137 4153 BY SIMILARITY.
 FT DOMAIN 4154 4170 BY SIMILARITY.
 FT DOMAIN 4171 4187 BY SIMILARITY.
 FT DOMAIN 4188 4204 BY SIMILARITY.
 FT DOMAIN 4205 4221 BY SIMILARITY.
 FT DOMAIN 4222 4238 BY SIMILARITY.
 FT DOMAIN 4239 4255 BY SIMILARITY.
 FT DOMAIN 4256 4272 BY SIMILARITY.
 FT DOMAIN 4273 4289 BY SIMILARITY.
 FT DOMAIN 4290 4306 BY SIMILARITY.
 FT DOMAIN 4307 4323 BY SIMILARITY.
 FT DOMAIN 4324 4340 BY SIMILARITY.
 FT DOMAIN 4341 4357 BY SIMILARITY.
 FT DOMAIN 4358 4374 BY SIMILARITY.
 FT DOMAIN 4375 4391 BY SIMILARITY.
 FT DOMAIN 4392 4408 BY SIMILARITY.
 FT DOMAIN 4409 4425 BY SIMILARITY.
 FT DOMAIN 4426 4442 BY SIMILARITY.
 FT DOMAIN 4443 4459 BY SIMILARITY.
 FT DOMAIN 4460 4476 BY SIMILARITY.
 FT DOMAIN 4477 4493 BY SIMILARITY.
 FT DOMAIN 4494 4510 BY SIMILARITY.
 FT DOMAIN 4511 4527 BY SIMILARITY.
 FT DOMAIN 4528 4544 BY SIMILARITY.
 FT DOMAIN 4545 4561 BY SIMILARITY.
 FT DOMAIN 4562 4578 BY SIMILARITY.
 FT DOMAIN 4579 4595 BY SIMILARITY.
 FT DOMAIN 4596 4612 BY SIMILARITY.
 FT DOMAIN 4613 4629 BY SIMILARITY.
 FT DOMAIN 4630 4646 BY SIMILARITY.
 FT DOMAIN 4647 4663 BY SIMILARITY.
 FT DOMAIN 4664 4680 BY SIMILARITY.
 FT DOMAIN 4681 4697 BY SIMILARITY.
 FT DOMAIN 4698 4714 BY SIMILARITY.
 FT DOMAIN 4715 4731 BY SIMILARITY.
 FT DOMAIN 4732 4748 BY SIMILARITY.
 FT DOMAIN 4749 4765 BY SIMILARITY.
 FT DOMAIN 4766 4782 BY SIMILARITY.
 FT DOMAIN 4783 4799 BY SIMILARITY.
 FT DOMAIN 4800 4816 BY SIMILARITY.
 FT DOMAIN 4817 4833 BY SIMILARITY.
 FT DOMAIN 4834 4850 BY SIMILARITY.
 FT DOMAIN 4851 4867 BY SIMILARITY.
 FT DOMAIN 4868 4884 BY SIMILARITY.
 FT DOMAIN 4885 4901 BY SIMILARITY.
 FT DOMAIN 4902 4918 BY SIMILARITY.
 FT DOMAIN 4919 4935 BY SIMILARITY.
 FT DOMAIN 4936 4952 BY SIMILARITY.
 FT DOMAIN 4953 4969 BY SIMILARITY.
 FT DOMAIN 4970 4986 BY SIMILARITY.
 FT DOMAIN 4987 5003 BY SIMILARITY.
 FT DOMAIN 5004 5020 BY SIMILARITY.
 FT DOMAIN 5021 5037 BY SIMILARITY.
 FT DOMAIN 5038 5054 BY SIMILARITY.
 FT DOMAIN 5055 5071 BY SIMILARITY.
 FT DOMAIN 5072 5088 BY SIMILARITY.
 FT DOMAIN 5089 5105 BY SIMILARITY.
 FT DOMAIN 5106 5122 BY SIMILARITY.
 FT DOMAIN 5123 5139 BY SIMILARITY.
 FT DOMAIN 5140 5156 BY SIMILARITY.
 FT DOMAIN 5157 5173 BY SIMILARITY.
 FT DOMAIN 5174 5190 BY SIMILARITY.
 FT DOMAIN 5191 5207 BY SIMILARITY.
 FT DOMAIN 5208 5224 BY SIMILARITY.
 FT DOMAIN 5225 5241 BY SIMILARITY.
 FT DOMAIN 5242 5258 BY SIMILARITY.
 FT DOMAIN 5259 5275 BY SIMILARITY.
 FT DOMAIN 5276 5292 BY SIMILARITY.
 FT DOMAIN 5293 5309 BY SIMILARITY.
 FT DOMAIN 5310 5326 BY SIMILARITY.
 FT DOMAIN 5327 5343 BY SIMILARITY.
 FT DOMAIN 5344 5360 BY SIMILARITY.
 FT DOMAIN 5361 5377 BY SIMILARITY.
 FT DOMAIN 5378 5394 BY SIMILARITY.
 FT DOMAIN 5395 5411 BY SIMILARITY.
 FT DOMAIN 5412 5428 BY SIMILARITY.
 FT DOMAIN 5429 5445 BY SIMILARITY.
 FT DOMAIN 5446 5462 BY SIMILARITY.
 FT DOMAIN 5463 5479 BY SIMILARITY.
 FT DOMAIN 5480 5496 BY SIMILARITY.
 FT DOMAIN 5497 5513 BY SIMILARITY.
 FT DOMAIN 5514 5530 BY SIMILARITY.
 FT DOMAIN 5531 5547 BY SIMILARITY.
 FT DOMAIN 5548 5564 BY SIMILARITY.
 FT DOMAIN 5565 5581 BY SIMILARITY.
 FT DOMAIN 5582 5598 BY SIMILARITY.
 FT DOMAIN 5599 5615 BY SIMILARITY.
 FT DOMAIN 5616 5632 BY SIMILARITY.
 FT DOMAIN 5633 5649 BY SIMILARITY.
 FT DOMAIN 5650 5666 BY SIMILARITY.
 FT DOMAIN 5667 5683 BY SIMILARITY.
 FT DOMAIN 5684 5700 BY SIMILARITY.
 FT DOMAIN 5701 5717 BY SIMILARITY.
 FT DOMAIN 5718 5734 BY SIMILARITY.
 FT DOMAIN 5735 5751 BY SIMILARITY.
 FT DOMAIN 5752 5768 BY SIMILARITY.
 FT DOMAIN 5769 5785 BY SIMILARITY.
 FT DOMAIN 5786 5802 BY SIMILARITY.
 FT DOMAIN 5803 5819 BY SIMILARITY.
 FT DOMAIN 5820 5836 BY SIMILARITY.
 FT DOMAIN 5837 5853 BY SIMILARITY.
 FT DOMAIN 5854 5870 BY SIMILARITY.
 FT DOMAIN 5871 5887 BY SIMILARITY.
 FT DOMAIN 5888 5904 BY SIMILARITY.
 FT DOMAIN 5905 5921 BY SIMILARITY.
 FT DOMAIN 5922 5938 BY SIMILARITY.
 FT DOMAIN 5939 5955 BY SIMILARITY.
 FT DOMAIN 5956 5972 BY SIMILARITY.
 FT DOMAIN 5973 5989 BY SIMILARITY.
 FT DOMAIN 5990 6006 BY SIMILARITY.
 FT DOMAIN 6007 6023 BY SIMILARITY.
 FT DOMAIN 6024 6040 BY SIMILARITY.
 FT DOMAIN 6041 6057 BY SIMILARITY.
 FT DOMAIN 6058 6074 BY SIMILARITY.
 FT DOMAIN 6075 6091 BY SIMILARITY.
 FT DOMAIN 6092 6108 BY SIMILARITY.
 FT DOMAIN 6109 6125 BY SIMILARITY.
 FT DOMAIN 6126 6142 BY SIMILARITY.
 FT DOMAIN 6143 6159 BY SIMILARITY.
 FT DOMAIN 6160 6176 BY SIMILARITY.
 FT DOMAIN 6177 6193 BY SIMILARITY.
 FT DOMAIN 6194 6210 BY SIMILARITY.
 FT DOMAIN 6211 6227 BY SIMILARITY.
 FT DOMAIN 6228 6244 BY SIMILARITY.
 FT DOMAIN 6245 6261 BY SIMILARITY.
 FT DOMAIN 6262 6278 BY SIMILARITY.
 FT DOMAIN 6279 6295 BY SIMILARITY.
 FT DOMAIN 6296 6312 BY SIMILARITY.
 FT DOMAIN 6313 6329 BY SIMILARITY.
 FT DOMAIN 6330 6346 BY SIMILARITY.
 FT DOMAIN 6347 6363 BY SIMILARITY.
 FT DOMAIN 6364 6380 BY SIMILARITY.
 FT DOMAIN 6381 6397 BY SIMILARITY.
 FT DOMAIN 6398 6414 BY SIMILARITY.
 FT DOMAIN 6415 6431 BY SIMILARITY.
 FT DOMAIN 6432 6448 BY SIMILARITY.
 FT DOMAIN 6449 6465 BY SIMILARITY.
 FT DOMAIN 6466 6482 BY SIMILARITY.
 FT DOMAIN 6483 6499 BY SIMILARITY.
 FT DOMAIN 6500 6516 BY SIMILARITY.
 FT DOMAIN 6517 6533 BY SIMILARITY.
 FT DOMAIN 6534 6550 BY SIMILARITY.
 FT DOMAIN 6551 6567 BY SIMILARITY.
 FT DOMAIN 6568 6584 BY SIMILARITY.
 FT DOMAIN 6585 6601 BY SIMILARITY.
 FT DOMAIN 6602 6618 BY SIMILARITY.
 FT DOMAIN 6619 6635 BY SIMILARITY.
 FT DOMAIN 6636 6652 BY SIMILARITY.
 FT DOMAIN 6653 6669 BY SIMILARITY.
 FT DOMAIN 6670 6686 BY SIMILARITY.
 FT DOMAIN 6687 6703 BY SIMILARITY.
 FT DOMAIN 6704 6720 BY SIMILARITY.
 FT DOMAIN 6721 6737 BY SIMILARITY.
 FT DOMAIN 6738 6754 BY SIMILARITY.
 FT DOMAIN 6755 6771 BY SIMILARITY.
 FT DOMAIN 6772 6788 BY SIMILARITY.
 FT DOMAIN 6789 6805 BY SIMILARITY.
 FT DOMAIN 6806 6822 BY SIMILARITY.
 FT DOMAIN 6823 6839 BY SIMILARITY.
 FT DOMAIN 6840 6856 BY SIMILARITY.
 FT DOMAIN 6857 6873 BY SIMILARITY.
 FT DOMAIN 6874 6890 BY SIMILARITY.
 FT DOMAIN 6891 6907 BY SIMILARITY.
 FT DOMAIN 6908 6924 BY SIMILARITY.
 FT DOMAIN 6925 6941 BY SIMILARITY.
 FT DOMAIN 6942 6958 BY SIMILARITY.
 FT DOMAIN 6959 6975 BY SIMILARITY.
 FT DOMAIN 6976 6992 BY SIMILARITY.
 FT DOMAIN 6993 7009 BY SIMILARITY.
 FT DOMAIN 7010 7026 BY SIMILARITY.
 FT DOMAIN 7027 7043 BY SIMILARITY.
 FT DOMAIN 7044 7060 BY SIMILARITY.
 FT DOMAIN 7061 7077 BY SIMILARITY.
 FT DOMAIN 7078 7094 BY SIMILARITY.
 FT DOMAIN 7095 7111 BY SIMILARITY.
 FT DOMAIN 7112 7128 BY SIMILARITY.
 FT DOMAIN 7129 7145 BY SIMILARITY.
 FT DOMAIN 7146 7162 BY SIMILARITY.
 FT DOMAIN 7163 7179 BY SIMILARITY.
 FT DOMAIN 7180 7196 BY SIMILARITY.
 FT DOMAIN 7197 7212 BY SIMILARITY.
 FT DOMAIN 7213 7229 BY SIMILARITY.
 FT DOMAIN 7230 7246 BY SIMILARITY.
 FT DOMAIN 7247 7263 BY SIMILARITY.
 FT DOMAIN 7264 7280 BY SIMILARITY.
 FT DOMAIN 7281 7297 BY SIMILARITY.
 FT DOMAIN 7298 7314 BY SIMILARITY.
 FT DOMAIN 7315 7331 BY SIMILARITY.
 FT DOMAIN 7332 7348 BY SIMILARITY.
 FT DOMAIN 7349 7365 BY SIMILARITY.
 FT DOMAIN 7366 7382 BY SIMILARITY.
 FT DOMAIN 7383 7399 BY SIMILARITY.
 FT DOMAIN 7400 7416 BY SIMILARITY.
 FT DOMAIN 7417 7433 BY SIMILARITY.
 FT DOMAIN 7434 7450 BY SIMILARITY.
 FT DOMAIN 7451 7467 BY SIMILARITY.
 FT DOMAIN 7468 7484 BY SIMILARITY.
 FT DOMAIN 7485 7501 BY SIMILARITY.
 FT DOMAIN 7502 7518 BY SIMILARITY.
 FT DOMAIN 7519 7535 BY SIMILARITY.
 FT DOMAIN 7536 7552 BY SIMILARITY.
 FT DOMAIN 7553 7569 BY SIMILARITY.
 FT DOMAIN 7570 7586 BY SIMILARITY.
 FT DOMAIN 7587 7603 BY SIMILARITY.
 FT DOMAIN 7604 7620 BY SIMILARITY.
 FT DOMAIN 7621 7637 BY SIMILARITY.
 FT DOMAIN 7638 7654 BY SIMILARITY.
 FT DOMAIN 7655 7671 BY SIMILARITY.
 FT DOMAIN 7672 7688 BY SIMILARITY.
 FT DOMAIN 7689 7705 BY SIMILARITY.
 FT DOMAIN 7706 7722 BY SIMILARITY.
 FT DOMAIN 7723 7739 BY SIMILARITY.
 FT DOMAIN 7740 7756 BY SIMILARITY.
 FT DOMAIN 7757 7773 BY SIMILARITY.
 FT DOMAIN 7774 7790 BY SIMILARITY.
 FT DOMAIN 7791 7807 BY SIMILARITY.
 FT DOMAIN 7808 7824 BY SIMILARITY.
 FT DOMAIN 7825 7841 BY SIMILARITY.
 FT DOMAIN 7842 7858 BY SIMILARITY.
 FT DOMAIN 7859 7875 BY SIMILARITY.
 FT DOMAIN 7876 7892 BY SIMILARITY.
 FT DOMAIN 7893 7909 BY SIMILARITY.
 FT DOMAIN 7910 7926 BY SIMILARITY.
 FT DOMAIN 7927 7943 BY SIMILARITY.
 FT DOMAIN 7944 7960 BY SIMILARITY.
 FT DOMAIN 7961 7977 BY SIMILARITY.
 FT DOMAIN 7978 7994 BY SIMILARITY.
 FT DOMAIN 7995 8011 BY SIMILARITY.
 FT DOMAIN 8012 8028 BY SIMILARITY.
 FT DOMAIN 8029 8045 BY SIMILARITY.
 FT DOMAIN 8046 8062 BY SIMILARITY.
 FT DOMAIN 8063 8079 BY SIMILARITY.
 FT DOMAIN 8080 8096 BY SIMILARITY.
 FT DOMAIN 8097 8112 BY SIMILARITY.
 FT DOMAIN 8113 8129 BY SIMILARITY.
 FT DOMAIN 8130 8146 BY SIMILARITY.
 FT DOMAIN 8147 8163 BY SIMILARITY.
 FT DOMAIN 8164 8180 BY SIMILARITY.
 FT DOMAIN 8181 8197 BY SIMILARITY.
 FT DOMAIN 8198 8214 BY SIMILARITY.
 FT DOMAIN 8215 8231 BY SIMILARITY.
 FT DOMAIN 8232 8248 BY SIMILARITY.
 FT DOMAIN 8249 8265 BY SIMILARITY.
 FT DOMAIN 8266 8282 BY SIMILARITY.
 FT DOMAIN 8283 8299 BY SIMILARITY.
 FT DOMAIN 8300 8316 BY SIMILARITY.
 FT DOMAIN 8317 8333 BY SIMILARITY.
 FT DOMAIN 8334 8350 BY SIMILARITY.
 FT DOMAIN 8351 8367 BY SIMILARITY.
 FT DOMAIN 8368 8384 BY SIMILARITY.
 FT DOMAIN 8385 8401 BY SIMILARITY.
 FT DOMAIN 8402 8418 BY SIMILARITY.
 FT DOMAIN 8419 8435 BY SIMILARITY.
 FT DOMAIN 8436 8452 BY SIMILARITY.
 FT DOMAIN 8453 8469 BY SIMILARITY.
 FT DOMAIN 8470 8486 BY SIMILARITY.
 FT DOMAIN 8487 8503 BY SIMILARITY.
 FT DOMAIN 8504 8520 BY SIMILARITY.
 FT DOMAIN 8521 8537 BY SIMILARITY.
 FT DOMAIN 8538 8554 BY SIMILARITY.
 FT DOMAIN 8555 8571 BY SIMILARITY.
 FT DOMAIN 8572 8588 BY SIMILARITY.
 FT DOMAIN 8589 8605 BY SIMILARITY.
 FT DOMAIN 8606 8622 BY SIMILARITY.
 FT DOMAIN 8623 8639 BY SIMILARITY.
 FT DOMAIN 8640 8656 BY SIMILARITY.
 FT DOMAIN 8657 8673 BY SIMILARITY.
 FT DOMAIN 8674 8690 BY SIMILARITY.
 FT DOMAIN 8691 8707 BY SIMILARITY.
 FT DOMAIN 8708 8724 BY SIMILARITY.
 FT DOMAIN 8725 8741 BY SIMILARITY.
 FT DOMAIN 8742 8758 BY SIMILARITY.
 FT DOMAIN 8759 8775 BY SIMILARITY.
 FT DOMAIN 8776 8792 BY SIMILARITY.
 FT DOMAIN 8793 8809 BY SIMILARITY.

FT	DISULFID	399	417	BY SIMILARITY.
FT	DISULFID	420	433	BY SIMILARITY.
FT	DISULFID	422	448	BY SIMILARITY.
FT	DISULFID	450	459	BY SIMILARITY.
FT	DISULFID	462	477	BY SIMILARITY.
FT	DISULFID	480	493	BY SIMILARITY.
FT	DISULFID	482	500	BY SIMILARITY.
FT	DISULFID	502	511	BY SIMILARITY.
FT	DISULFID	514	528	BY SIMILARITY.
FT	DISULFID	791	803	BY SIMILARITY.
FT	DISULFID	793	810	BY SIMILARITY.
FT	DISULFID	812	821	BY SIMILARITY.
FT	DISULFID	824	836	BY SIMILARITY.
FT	DISULFID	839	851	BY SIMILARITY.
FT	DISULFID	841	858	BY SIMILARITY.
FT	DISULFID	860	869	BY SIMILARITY.
FT	DISULFID	872	882	BY SIMILARITY.
FT	DISULFID	885	894	BY SIMILARITY.
FT	DISULFID	887	901	BY SIMILARITY.
FT	DISULFID	904	913	BY SIMILARITY.
FT	DISULFID	916	932	BY SIMILARITY.
FT	DISULFID	935	951	BY SIMILARITY.
FT	DISULFID	937	962	BY SIMILARITY.
FT	DISULFID	964	973	BY SIMILARITY.
FT	DISULFID	976	990	BY SIMILARITY.
FT	DISULFID	993	1007	BY SIMILARITY.
FT	DISULFID	995	1014	BY SIMILARITY.
FT	DISULFID	1017	1026	BY SIMILARITY.
FT	DISULFID	1029	1042	BY SIMILARITY.
FT	DISULFID	1045	1059	BY SIMILARITY.
FT	DISULFID	1047	1066	BY SIMILARITY.
FT	DISULFID	1068	1077	BY SIMILARITY.
FT	DISULFID	1080	1093	BY SIMILARITY.
FT	DISULFID	1096	1108	BY SIMILARITY.
FT	DISULFID	1098	1115	BY SIMILARITY.
FT	DISULFID	1117	1126	BY SIMILARITY.
FT	DISULFID	1129	1141	BY SIMILARITY.
FT	DISULFID	1144	1156	BY SIMILARITY.
FT	DISULFID	1146	1163	BY SIMILARITY.
FT	DISULFID	1165	1174	BY SIMILARITY.
FT	DISULFID	1177	1188	BY SIMILARITY.
FT	DISULFID	1191	1191	INTERCHAIN (PROBABLE).
FT	DISULFID	1194	1194	INTERCHAIN (PROBABLE).
FT	DISULFID	1788	1788	INTERCHAIN (PROBABLE).
FT	SITE	643	645	CELL ATTACHMENT SITE (POTENTIAL).
FT	CARBOHYD	140	140	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	203	203	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	234	234	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	489	489	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	593	593	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1053	1053	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1248	1248	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1303	1303	N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match 7.4%; Score 173; DB 1; Length 1790;

Best Local Similarity 21.5%; Pred. No. 0.00017;

Matches 97; Conservative 37; Mismatches 147; Indels 170; Gaps 23;

QY	10	IISLFINELRAVPC	---PDGTTQAGLTDVGAADLGTVCNCRPNFYNGGAQGEANGNQ	66
Db	779	ILSVFVHD	-GASMCNCPMTGS-----LSKVESNGGYC-QCKPNV--GRQCDQCAPGT	829
QY	67	PFAANNAARGICVPC	INRVGSVTNAGDLATLATQCTGCTGATLDDGVTDVDFDRSAQ	126
Db	830	GFGPEG	-----CRACDCNSIGSKDKYCDLITGQCQC	868
QY	127	CVCKKPNFYNGSG	POGEAPGVQVFAAGAAAGAAVTSQCPQCLNKNDSPATAGAA	186
Db	869	CNOCQPGYW	-----NFPCECRVCQCNHGAATCDPIQGTCDICQ	907
QY	187	LATQCSNQCTGT	VLDGVTLVFNTSATLCVKCRPNFYNG--GSPQGEAPGVQVFAAGA	244
Db	908	-----	-----TTGYSDCSLDGYGNPLFGSEIG-----	931

```

DR EMBL: AF079520: AAD29851.1; -.
DR HSP; P02468; iKLO.
DR MGD; MGI:1344394; Lamc3.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001886; LaminT.
DR InterPro; IPR000034; Laminin_B.
DR InterPro; IPR002049; Laminin_EGF.
DR Pfam; PF00052; laminin_B; 1.
DR Pfam; PF00053; laminin_EGF; 10.
DR Pfam; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGF_LAMININ.
DR PDom; PD002082; LaminT; 1.
DR SMART; SM00180; EGF_Lam; 10.
DR SMART; SM00281; LamB; 1.
DR SMART; SM00136; LaminT; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_8.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 11.
DR Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
FT SIGNAL 1 28
FT CHAIN 29 1581
FT DOMAIN 29 279 LAMININ GAMMA-3 CHAIN.
FT DOMAIN 280 335 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 336 391 LAMININ EGF-LIKE 1.
FT DOMAIN 392 438 LAMININ EGF-LIKE 2.
FT DOMAIN 439 488 LAMININ EGF-LIKE 3.
FT DOMAIN 489 498 LAMININ EGF-LIKE 4.
FT DOMAIN 499 584 LAMININ EGF-LIKE 5 (N-TERMINAL).
FT DOMAIN 585 718 LAMININ DOMAIN IV.
FT DOMAIN 719 766 LAMININ EGF-LIKE 5 (C-TERMINAL).
FT DOMAIN 767 821 LAMININ EGF-LIKE 6.
FT DOMAIN 822 877 LAMININ EGF-LIKE 7.
FT DOMAIN 878 927 LAMININ EGF-LIKE 8.
FT DOMAIN 928 975 LAMININ EGF-LIKE 9.
FT DOMAIN 976 1024 LAMININ EGF-LIKE 10.
FT DOMAIN 1025 1581 LAMININ EGF-LIKE 11.
FT DOMAIN 1029 1046 LAMININ II AND I.
FT DOMAIN 1112 1153 COILED COIL (POTENTIAL).
FT DOMAIN 1208 1231 COILED COIL (POTENTIAL).
FT DOMAIN 1438 1468 COILED COIL (POTENTIAL).
FT DOMAIN 1510 1575 COILED COIL (POTENTIAL).
FT CARBOHYD 128 128 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 304 304 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 337 337 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 640 640 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 849 849 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 991 991 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1162 1162 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1196 1196 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1320 1320 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1514 1514 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 9 9 L -> F (IN REF. 2).
FT CONFLICT 190 190 P -> T (IN REF. 2).
FT CONFLICT 195 195 R -> K (IN REF. 2).
FT CONFLICT 221 221 G -> S (IN REF. 2).
FT CONFLICT 394 394 C -> R (IN REF. 2).
FT CONFLICT 471 471 C -> Y (IN REF. 2).
FT CONFLICT 1150 1150 L -> LDEPOLFSLKK (IN REF. 2).
FT CONFLICT 1387 1387 H -> O (IN REF. 2).
FT CONFLICT 1438 1439 AS -> YI (IN REF. 2).
FT CONFLICT 1479 1479 V -> I (IN REF. 2).
SQ SEQUENCE 1581 AA; 172316 MW; 51DFAD1F95E6AE81 CRC64;

Query Match
Best Local Similarity 7.4%; Score 172.5; DB 1; Length 1581;
Matches 86; Conservative 40; Mismatches 131; Indels 159; Gaps 26;

QY 21 VPCPDGTQTQAGLTD--VGAADLG-----TCVNCRPNFYNGGAAQGEANGNPFAANN 72
DB 717 IPC---TCNQHGTCDPNTGICLGHHTGEGSCRCMPGFY--GNAFSGRADDCQP----- 766
QY 73 AARGICVPCQ--INRVGSVTNAGDLATLATQCSTQCPTGTALDDGVTDFDRSAOCVKCK 131

```

```

Db 767 -----CPCPGQACATIPESGDVV-----CTHCPPG-----ORGRRCESCE 802
QY 132 PNFYNGGSPQGEAPGVQVFAAGAAAAGVAAVTSCVPCQLNKNKNDSPATAGAAQANLATQC 191
Db 803 DGFF---GDP-----LGLSGAPQPCRCQCQSGN-----VDLNAVNC 836
QY 192 ---SNQCPTGTVLDGVTLVFNTSATLCVKCRPNFYNGGSPQGEAPGVQVFAAGAAAAG 248
Db 837 DPHSGHC-----LRCLYNTTGAHCEHCREGFY-----GSAYA- 868
QY 249 VAAVTSCVPCQIN-----KNDSPATAGAAQANLATQCSTQCPTGTALDQGVTLVESNS 301
Db 869 -TRPVDKCAPCSCDLRGSVSEKTCNPVTG-----QC-----VCLPYV-S 905
QY 302 STQCSOCIANYFFNGFNFAKQSKLKCVPKTPPAHAPGNTATQAT-OCLTTCPTAGTVLD 360
Db 906 GRDCSRCSFGFY---DLQSRG-CQSC---KCHPLGSLKCHPKTGQC--PCRPQ---- 952
QY 361 DGTSTNFVASATECTKCSAGFFASKTTGFTAGTDTCTCTCKLITSGATAKYVAEAT 416
Db 953 -----VTGQACDRCLGFFGFSIKG-----CRDCRCSPLGAASSQCHENST 993

```

Search completed: February 11, 2003, 19:46:54
Job time : 20.7429 secs